

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: SPARKS, Andrew B.
HOFFMAN, Noah
KAY, Brian K.
FOWLKES, Dana M.
McCONNELL, Stephen J.

(ii) TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND USING SAME

(iii) NUMBER OF SEQUENCES: 227

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/630,915
(B) FILING DATE: 03-APR-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Misrock, S. Leslie
(B) REGISTRATION NUMBER: 18,872
(C) REFERENCE/DOCKET NUMBER: 1101-174

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Other

(D) OTHER INFORMATION: May or may not have carboxy-terminal amide and/or biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ser Gly Ser Gly Gly Ile Leu Ala Pro Pro Val Pro Pro Arg Asn Thr
1 5 10 15

Arg

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: Other
(D) OTHER INFORMATION: May or may not have carboxy-terminal amide and/or biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ser Gly Ser Gly Ser Arg Leu Thr Pro Gln Ser Lys Pro Pro Leu Pro
1 5 10 15

Pro Lys Pro Ser Trp Val Ser Arg
20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: Other
(D) OTHER INFORMATION: May or may not have carboxy-terminal amide and/or biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Ile Leu Ala Pro Pro Val Pro Pro Arg Asn Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: Other
(D) OTHER INFORMATION: May or may not have carboxy-terminal amide and/or biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Val Leu Lys Arg Pro Leu Pro Ile Pro Pro Val Thr Arg

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTGAATGCTG CAGACAGTGA CGGATGGACA CCACTGCATT GTGCTGCCTC TTGCAACAGT	60
GTCCACCTCT GCAAGCAGCT GGTGGAAAGT GGAGCCGCTA TCTTGCCTC CACCATCAGT	120
GACATTGAGA CTGCTGCAGA CAAGTGTGAA GAGATGGAAG AGGGATACAT CCAGTGTTC	180
CAGTTCTGT ATGGGGTACA AGAGAAGCTG GGAGTGATGA ACAAAGGCAC CGTGTATGCT	240
TTGTGGGACT ACGAGGCCA GAACAGCGAT GAGCTGCCT TCCATGAAGG GGATGCCATC	300
ACCATCCTGA GCGCAAAGA TGAAAACGAG ACCGAGTGGT GGTGGCTCG TCTTGGGGAC	360
CGGGAGGGCT ACGTGCCAA AAACTTGCTG GGGTTGTATC CACGGATCAA ACCCCGGCAG	420
CGAACACTTG CCTGAACCCC CTGGAGTACC ACAGTCTCGT TTGCTCCCAG GAGCTACTGG	480
AGGAGATCCC ACTGCCCTGG GAAAACGTAA GCTAGGATGG TCTCCTGGTG CTCACTTTAG	540
CAGACAGTGT CCACAATGTG AATCCCACCTT CCCAGGTGAG GCCCTCTCCA GGCTGCAGGA	600
GCTGG	605

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Val Asn Ala Ala Asp Ser Asp Gly Trp Thr Pro Leu His Cys Ala Ala			
1	5	10	15
Ser Cys Asn Ser Val His Leu Cys Lys Gln Leu Val Glu Ser Gly Ala			
20	25	30	
Ala Ile Phe Ala Ser Thr Ile Ser Asp Ile Glu Thr Ala Ala Asp Lys			
35	40	45	
Cys Glu Glu Met Glu Glu Gly Tyr Ile Gln Cys Ser Gln Phe Leu Tyr			
50	55	60	
Gly Val Gln Glu Lys Leu Gly Val Met Asn Lys Gly Thr Val Tyr Ala			
65	70	75	80
Leu Trp Asp Tyr Glu Ala Gln Asn Ser Asp Glu Leu Ser Phe His Glu			
85	90	95	

Gly Asp Ala Ile Thr Ile Leu Arg Arg Lys Asp Glu Asn Glu Thr Glu
 100 105 110
 Trp Trp Trp Ala Arg Leu Gly Asp Arg Glu Gly Tyr Val Pro Lys Asn
 115 120 125
 Leu Leu Gly Leu Tyr Pro Arg Ile Lys Pro Arg Gln Arg Thr Leu Ala
 130 135 140

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1277 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAATTCAAGC	TCGGGTTGCG	CGCGGTCCGG	AGCGGCCGCG	GCCAGCCAG	GCTTGGCGCC	60
CAGTTGTCGT	GTGCGTGTGG	GGCTCCCGCG	GCTGAGCCTG	GTCGCTCCGT	GTAGCGCCAT	120
GTCCAAGCCA	CCTCCCAAAC	CGGTCAAACC	AGGGCAAGTT	AAAGTCTTCA	GAGCTCTATA	180
TACATTTGAA	CCCAGAACTC	CAGATGAATT	ATACTTGAA	GAAGGAGACA	TTATCTACAT	240
CACTGACATG	AGTGATACCA	GCTGGTGGAA	AGGGACATGC	AAGGGCAGAA	CAGGACTGAT	300
CCCGAGCAAC	TATGTGGCTG	AGCAGGCAGA	ATCCATTGAC	AATCCATTGC	ATGAAGCTGC	360
AAAAAGAGGC	AACCTGAGCT	GGTTGAGGGA	GTGCTTGGAC	AACCGGGTGG	GTGTGAACGG	420
CCTGGACAAA	GCTGGAAGCA	CAGCCCTGTA	CTGGGCCTGC	CACGGTGGCC	ATAAAGACAT	480
AGTGGAGGTT	CTGTTTACTC	AGCCGAATGT	GGAGCTGAAC	CAGCAGAATA	AGCTGGGAGA	540
CACAGCTCTG	CACGCGGNTG	CCTGGAAGGG	TTATGCAGAC	ATTGTCAGT	TGCTACTGGC	600
AAAAGGTGCG	AGGACAGACT	TGAGAAACAA	TGAGAAGAAG	CTGGCCTTGG	ACATGGCCAC	660
CAACGCTGCC	TGTGCATCGC	TCCTGAAGAA	GAAGCAGCAG	GGAACAGATG	GGGCTCGAAC	720
GTAAAGCAAC	GCCGAGGACT	ACCTCGATGA	CGAAGACTCA	GACTGATTCC	CCCCGGGGCC	780
GCTTGATTG	TTGCCTAAC	TTCTTTGCT	TTTGCCATTG	CGGAGCCTGG	GTTGTTGCC	840
AGAAAGAGTAT	TGATAACTGT	TGCTTTAAA	GTCTGTATGA	GCGCGACACT	GCTGCACTGT	900
GATCTGTGAG	GAGTCGTTGT	GAGGGTGGCT	CATTCTCACC	CACGCCTTGN	CAATAAGTGA	960
AGAGATACTT	TGTTGTATAA	AATACATATA	TGCTCACCA	GGTAAAATAA	ACGAAAAAAA	1020
NTTATTTCTA	TTTATCAAGC	AAAAAAGAAA	AAGCTTGGGC	CCTNTTCTAT	AGTGTACCT	1080
AAATACTAGC	TTGANCCGGN	TGCTAACAAA	GCCCGAAAGG	AAGCTGAGTT	GCTGCTGCCA	1140
CCGNTGAGCA	ATAACTAGCA	TANCCCCTTG	GGGCCTCTAA	ACGGGTCTTG	AGGGGTTTTT	1200
NGNTGAAAGG	AGGANCTATT	TCCGGATAAC	CTGGNGTAAT	AGGGAAGAGG	CCCGNACCGA	1260
TCGCCCTTCC	CAACAGA					1277

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Gly Cys Ala Arg Ser Gly Ala Ala Ala Ala Ser Ala Gly Leu Ala
1 5 10 15

Pro Ser Cys Arg Val Arg Val Gly Leu Pro Arg Leu Ser Leu Val Ala
20 25 30

Pro Cys Ser Ala Met Ser Lys Pro Pro Pro Lys Pro Val Lys Pro Gly
35 40 45

Gln Val Lys Val Phe Arg Ala Leu Tyr Thr Phe Glu Pro Arg Thr Pro
50 55 60

Asp Glu Leu Tyr Phe Glu Glu Gly Asp Ile Ile Tyr Ile Thr Asp Met
65 70 75 80

Ser Asp Thr Ser Trp Trp Lys Gly Thr Cys Lys Gly Arg Thr Gly Leu
85 90 95

Ile Pro Ser Asn Tyr Val Ala Glu Gln Ala Glu Ser Ile Asp Asn Pro
100 105 110

Leu His Glu Ala Ala Lys Arg Gly Asn Leu Ser Trp Leu Arg Glu Cys
115 120 125

Leu Asp Asn Arg Val Gly Val Asn Gly Leu Asp Lys Ala Gly Ser Thr
130 135 140

Ala Leu Tyr Trp Ala Cys His Gly Gly His Lys Asp Ile Val Glu Val
145 150 155 160

Leu Phe Thr Gln Pro Asn Val Glu Leu Asn Gln Gln Asn Lys Leu Gly
165 170 175

Asp Thr Ala Leu His Ala Ala Ala Trp Lys Gly Tyr Ala Asp Ile Val
180 185 190

Gln Leu Leu Ala Lys Gly Ala Arg Thr Asp Leu Arg Asn Asn Glu
195 200 205

Lys Lys Leu Ala Leu Asp Met Ala Thr Asn Ala Ala Cys Ala Ser Leu
210 215 220

Leu Lys Lys Gln Gln Gly Thr Asp Gly Ala Arg Thr Leu Ser Asn
225 230 235 240

Ala Glu Asp Tyr Leu Asp Asp Glu Asp Ser Asp
245 250

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACTCACGNCG GTGGAGTGGT ACCGGATCGA ATTCAAGCCG CATCACTGGC ACTGGACGCC	60
AGGGCATCTT CCCTGCCAGC TACGTGCAGA TAAACCGAGA GCCCCGGCTC AGGCTTTGTG	120
ATGATGGTCC CCAGCTCCCT GCATCACCTA ACCCGACAAC CACTGCTCAC CTAAGCAGCC	180
ACTCCCACCC CTCCTCAATA CCTGTGGACC CCACTGACTG GGGAGGTGCA ACCTCCCCTC	240
GACGCTCCGC CTTTCCCTTC CCCATCACCC TCCAGGAGCC CAGATCCAA ACCCAGAGTC	300
TCAATAACCC TGGACCAACC CTGTCCCATC CTGGAGGCCAC CAGCCGTCCC ATAACCTGG	360
GACCCTCCTC CCCAAACACA GAGATACACT GGACTCCGTA CGGGGCCATG TACCAAGTACA	420
GGCCCCAGAA TGAGGACGAG CTGGAACCTTC GAGAGGGGA CCGTGTGGAT GTCATGCAGC	480
AATGTGACGA TGGCTGGTTT GTGGGTGTCT CCCGGCGAAC TCAGAAATTG GGGACATTCC	540
CTGGAAATTA TGTAGCCCCA GTGTGAGTGG TCTCCATGGC AGTTGGAGC CAACGAGGAT	600
CGGGAGGGGA GCAGTAGCAC TATGGGAGGG AGAGAGGCCT TCCATAGCCT CCTCCCCAGG	660
ACCTGTGCTC CCAGCTTCTG CAGAGACCCC AGCAACTTTC CCTCCAAGCC TCCTTGAAGT	720
CCGATTCCCCA CCCCGCAAGT CACAGGCATT CCTTGACAG CCCCTTCAC CGCCCCCTCAA	780
ATACAGACAT CTGCTTCAT GTGGGNAAAA AAAAAAAATT AAAAGGTGGC CCTAT	835

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Arg Ile Thr Gly Thr Gly Arg Gln Gly Ile Phe Pro Ala Ser Tyr Val			
1	5	10	15
Gln Ile Asn Arg Glu Pro Arg Leu Arg Leu Cys Asp Asp Gly Pro Gln			
20	25	30	
Leu Pro Ala Ser Pro Asn Pro Thr Thr Thr Ala His Leu Ser Ser His			
35	40	45	
Ser His Pro Ser Ser Ile Pro Val Asp Pro Thr Asp Trp Gly Gly Arg			
50	55	60	
Thr Ser Pro Arg Arg Ser Ala Phe Pro Phe Pro Ile Thr Leu Gln Glu			
65	70	75	80
Pro Arg Ser Gln Thr Gln Ser Leu Asn Thr Pro Gly Pro Thr Leu Ser			
85	90	95	
His Pro Arg Ala Thr Ser Arg Pro Ile Asn Leu Gly Pro Ser Ser Pro			
100	105	110	

Asn	Thr	Glu	Ile	His	Trp	Thr	Pro	Tyr	Arg	Ala	Met	Tyr	Gln	Tyr	Arg
115							120					125			
Pro	Gln	Asn	Glu	Asp	Glu	Leu	Glu	Leu	Arg	Glu	Gly	Asp	Arg	Val	Asp
130					135					140					
Val	Met	Gln	Gln	Cys	Asp	Asp	Gly	Trp	Phe	Val	Gly	Val	Ser	Arg	Arg
145						150				155			160		
Thr	Gln	Lys	Phe	Gly	Thr	Phe	Pro	Gly	Asn	Tyr	Val	Ala	Pro	Val	
					165				170				175		

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2143 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTNNNNYYMM SKYSKKGKKK KGKWMMSGRTC GATTCAAGCC GACCAGCGGC GGCCCGGGCGA	60
CCCCAGCCGC CTCTCCGCAT CTGCATCTGC ATCTGCCGGC CGCGCAGCCT CCCGCATCCC	120
ATCATGTCGG TGGCAGGGCT GAAGAAGCAG TTCCACAAAG CCACTCAGAA AGTGAGTGAG	180
AAGGTGGGAG GAGCGGAAGG CACCAAGCTC GATGATGACT TCAAAGAGAT GGAGAGGAAA	240
GTGGATGTCA CCAGCAGGGC TGTGATGGAG ATAATGACAA AAACGATTGA ATACCTCCAA	300
CCCAATCCAG CTTCCAGGGC TAAGCTCAGT ATGATCAACA CCATGTCGAA AATCCGCGGC	360
CAAGAGAAGG GGCCAGGCTA CCCTCAGGCG GAAGCACTGC TGGCAGAGGC CATGCTCAAG	420
TTCCGGCAGGG AGCTGGGTGA TGATTGCAAC TTTGGTCCTG CTCTCGGTGA GGTGGGAGAA	480
GCCATGAGGG AGCTCTCGGA GGTCAAGGAC TCATTGGACA TGGAAAGTGAA GCAGAATTTC	540
ATCGACCCCC TTCAGAATCT TCATGACAAG GATCTGAGGG AGATTCAAGCA TCATCTGAAA	600
AAGCTGGAAG GCCGACGCTT AGACTTTGGT TATAAGAAGA AGCGACAAGG CAAGATTCCA	660
GATGAAGAAC TCCGCCAACG TCTGGAGAAA TTGATGAGT CTAAAGAAAT CGCCGAGTCG	720
AGCATGTTCA ACCTCTTGGA GATGGATATA GAACAGGTGA GCCAGCTCTC CGCACCTGTT	780
CAGGCTCAGC TGGAGTACCA CAAGCAGGCC GTGCAGATCC TGCAGCAGGT CACTGTCAGA	840
CTGGAAGAAA GAATAAGACA AGCTTCATCT CAGCCAAGAA GGGAAATATCA GCCCAAACCA	900
CGGATGAGCC TAGAGTTGC CACTGGAGAC AGTACTCAGC CCAACGGGG TCTCTCCCAC	960
ACAGGCACAC CCAAACCTCC AGGTGTCCAA ATGGATCAGC CCTGCTGCCG AGCTCTGTAT	1020
GACTTGGAAC CTGAAAATGA AGGGGAATTG GCTTTAAAG AGGGCGATAT CATCACACTC	1080
ACTAATCAGA TTGACCGAGAA CTGGTATGAG GGGATGCTTC ATGGCCAGTC TGGCTTTTC	1140
CCCATCAACT ATGTAGAAAT TCTGGTTGCT CTGCCCTATT AGGATCCTGT GCTGGCTGGC	1200
TCACCTCCTT CTGACCCAGA TAGTTAAGTT TAACCACTGC TTTGGTAATG CTGCTTCCAA	1260

TACATCACGA ATGCAGGCCG CAGTGGATGA GTCACCAAGC CCACACGTGC CCTGGGTTGA	1320
CCCGTGTGCT CCTCCAGGAG ACGCGGTGAT AGATGGTATC TTCCAAGGCC AGTGGGCCTG	1380
GTACATGCTT TAAAACACCA TCTGAGACTA GCCAGGAGTC CCAGAACTGG CTTCACAGTT	1440
CTCAGGAGGC TGTGGTTCCCT GGTAAACATGC CTGTGAACCA CATGGCAGAA AAACTCTCCT	1500
CACTGAAGAT ATTGTCTCTC ACCCAGGGC CATCTCAAGG TCTCCAGTTC TCCATTTACA	1560
GAGGAGAAAG TCCTTTTGT TGCACTTCC CTTCCTAAAT ATGTGAGTCA CAGAATTGTT	1620
GGCAAAAACA TCCCCTCACC AGCAAGATGT CTGCTGGTTT AAGCAACTTG GTCTCTTGAT	1680
GCCATTAGCA AAAGTATTAA TTGTCCAAAG CACCTTGTT CACTAATATC TATCTATCTA	1740
TCTATCTATC TATCTATCTA TCTATCTATC TATCTATCAT CTATCTACCT ACCTATCTAC	1800
CTATCATCTA TCTATCTATC ATCTATTATC TATCTATCTA TCTATCTATC NNTCNATCTA	1860
TCTATCTATC CATCTATCTA TCCATCATCT ATCTACCTAC CTATCTACTA TCCATCTATC	1920
TATCTATCCA TCATCTATCT ACCTACCTAT CTACTATCCA TCCATTATC TATCTATCTA	1980
TCTATCTATC TATCTATCTA TCTCCCTCAT ACTTCTGAGA CATGGCCAGT TTTCTTCCCT	2040
CCCTGCTGTT AAGCACTTGG NAGATGAGGG GGGGGTCCC ATTTNATTTC TGAGTGAGAT	2100
GGTGAGCAGG GTGTATGTTG GCTGTNNNTNN GGGGGTGGCC CTA	2143

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Ser	Val	Ala	Gly	Leu	Lys	Gln	Phe	His	Lys	Ala	Thr	Gln	Lys	
1				5				10				15			
Val	Ser	Glu	Lys	Val	Gly	Gly	Ala	Glu	Gly	Thr	Lys	Leu	Asp	Asp	Asp
		20					25					30			
Phe	Lys	Glu	Met	Glu	Arg	Lys	Val	Asp	Val	Thr	Ser	Arg	Ala	Val	Met
	35					40						45			
Glu	Ile	Met	Thr	Lys	Thr	Ile	Glu	Tyr	Leu	Gln	Pro	Asn	Pro	Ala	Ser
	50					55				60					
Arg	Ala	Lys	Leu	Ser	Met	Ile	Asn	Thr	Met	Ser	Lys	Ile	Arg	Gly	Gln
	65				70				75						80
Glu	Lys	Gly	Pro	Gly	Tyr	Pro	Gln	Ala	Glu	Ala	Leu	Leu	Ala	Glu	Ala
		85					90						95		
Met	Leu	Lys	Phe	Gly	Arg	Glu	Leu	Gly	Asp	Asp	Cys	Asn	Phe	Gly	Pro
		100					105						110		
Ala	Leu	Gly	Glu	Val	Gly	Glu	Ala	Met	Arg	Glu	Leu	Ser	Glu	Val	Lys
		115					120						125		

Asp Ser Leu Asp Met Glu Val Lys Gln Asn Phe Ile Asp Pro Leu Gln
 130 135 140

Asn Leu His Asp Lys Asp Leu Arg Glu Ile Gln His His Leu Lys Lys
 145 150 155 160

Leu Glu Gly Arg Arg Leu Asp Phe Gly Tyr Lys Lys Lys Arg Gln Gly
 165 170 175

Lys Ile Pro Asp Glu Glu Leu Arg Gln Ala Leu Glu Lys Phe Asp Glu
 180 185 190

Ser Lys Glu Ile Ala Glu Ser Ser Met Phe Asn Leu Leu Glu Met Asp
 195 200 205

Ile Glu Gln Val Ser Gln Leu Ser Ala Leu Val Gln Ala Gln Leu Glu
 210 215 220

Tyr His Lys Gln Ala Val Gln Ile Leu Gln Gln Val Thr Val Arg Leu
 225 230 235 240

Glu Glu Arg Ile Arg Gln Ala Ser Ser Gln Pro Arg Arg Glu Tyr Gln
 245 250 255

Pro Lys Pro Arg Met Ser Leu Glu Phe Ala Thr Gly Asp Ser Thr Gln
 260 265 270

Pro Asn Gly Gly Leu Ser His Thr Gly Thr Pro Lys Pro Pro Gly Val
 275 280 285

Gln Met Asp Gln Pro Cys Cys Arg Ala Leu Tyr Asp Leu Glu Pro Glu
 290 295 300

Asn Glu Gly Glu Leu Ala Phe Lys Glu Gly Asp Ile Ile Thr Leu Thr
 305 310 315 320

Asn Gln Ile Asp Glu Asn Trp Tyr Glu Gly Met Leu His Gly Gln Ser
 325 330 335

Gly Phe Phe Pro Ile Asn Tyr Val Glu Ile Leu Val Ala Leu Pro His
 340 345 350

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1867 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGGGCGCGGC	GGGAGCCTGG	TGGACCTGTC	TTGGCGGTA	ATCATTGATC	ATCGCAGATG	60
CCCTCATATC	CACTTGGAT	TCCTTGGATT	CGGACAGACT	CTGAACTGCT	TTTCCCAGCA	120
AAAGAGAAAG	ATGTGGAAAG	CCTCTGCAGG	CCATGCTGTG	TCCATCACGC	AGGATGATGG	180
AGGAGCTGAT	GACTGGGAGA	CTGATCCTGA	TTTGTGAAT	GATGTGAGTG	AAAAGGAGCA	240
GAGATGGGT	GCTAAAACCG	TGCAGGGATC	GGGGCACCAAG	GAACACATCA	ACATTCACAA	300
GCTTCGAGAG	AATGTCTTCC	AAGAACACCA	GACGCTCAAG	GAGAAGGAGC	TGGAAACGGG	360

ACCCAAGGCT	TCCCACGGCT	ATGGCGGAA	GTTCGGTGTG	GAGCAGGATA	GGATGGACAG	420
ATCAGCCGTG	GGCCATGAGT	ACCAAGTCGAA	GCTTTCCAAG	CACTGCTCAC	AAGTGGACTC	480
GGTCCGGGGC	TTCGGAGGCA	AGTTCGGTGT	CCAGATGGAC	AGGGTGGATC	AGTCTGCTGT	540
AGGCTTGAA	TACCAGGGGA	AGACTGAGAA	GCATGCCTCC	CAGAAAGACT	ACTCTAGTGG	600
CTTCGGTGGC	AAATACGGTG	TGCAAGCTGA	CCGTGTAGAC	AAGAGTGCCG	TGGGCTTTGA	660
CTACCAGGGC	AAGACGGAGA	AGCATGAGTC	TCAGAAAGAT	TAECTCAAAG	GTTTTGGTGG	720
CAAATATGGG	ATTGACAAGG	ACAAGGTGGA	TAAAAGTCCT	GTGGGCTTTG	AGTATCAAGG	780
CAAGACAGAG	AAGCACGAAT	CCCAGAAAGA	CTATGTAAAA	GGCTTTGGAG	GAAAGTTGG	840
TGTGCAGACA	GACAGACAGG	ACAAGTGTGC	CCTTGGCTGG	GACCATCAGG	AGAAGCTGCA	900
GCTGCATGAA	TCCCAGAAAG	ACTATAAGAC	TGGTTTCGGA	GGCAAATTG	GTGTTCAGTC	960
CGAGAGGCAG	GACTCCTCCG	CTGTGGGGTT	TGATTACAAG	GAGAGATTGG	CCAAGCACGA	1020
GCCCCAGCAA	GAATATGCCA	AAGGATTCGG	CGGGAAAGTAT	GGGGTGCAGA	AGGATCGGAT	1080
GGACAAGAAAT	GCATCCACCT	TTGAAGAAGT	GGTCCAGGTG	CCATCTGCCT	ATCAGAAGAC	1140
TGTCCCCATT	GAGGCCGTAA	CCAGCAAAAC	CAGTAATATC	CGTGTAACT	TTGAAAACCT	1200
GGCAAAGGAG	AGAGAGCAGG	AGGACAGGCG	GAAGGCAGAA	GCCGAGAGAG	CTCAGCGGAT	1260
GGCCAAAGAA	AGACAGGAGC	AGGAGGAGGC	GCCGAGGAAG	CTGGAAGAGC	AAGCCAGAGC	1320
CAAGAACAG	ACGCCCCCTG	CATCCCCTAG	TCCTCAACCA	ATTGAAGACA	GACCACCCCTC	1380
CAGCCCCATC	TATGAGGATG	CAGCTCCGTT	CAAGGCGAG	CCGAGCTACC	GAGGTAGCGA	1440
ACCTGAGCCT	GAGTACAGCA	TCGAGGCCGC	AGGCATTCCCT	GAGGCTGGCA	GCCAGCAAGG	1500
CCTGACCTAT	ACATCAGAGC	CCGTGTACGA	GAATACAGAG	GCTCCTGGCC	ACTATCAAGC	1560
AGAGGATGAC	ACCTACGATG	GGTATGAGAG	TGACCTGGGC	ATCACAGCCA	TCGCCCTGTA	1620
TGACTTACAG	GCTGCTGGCG	ATGATGAGAT	CTCCTTGAC	CCTGATGACA	TCATCACCAA	1680
CATAGAAATG	ATTGACGATG	GCTGGTGGCG	TGGGGTGTGC	AAGGGCAGAT	ACGGGCTCTT	1740
CCCAGCCAAG	TATGTGGAGC	TGCGGCAGTA	GGGCTGCCAC	CCAGAGCCTA	CCGGCACCAAG	1800
CACAGGGTTC	ACACTACAGA	GCATCTGGGT	GTGTTGAGT	TGGTTTCTGC	TTCCGTTTCT	1860
GT	TTTTG					1867

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Trp	Lys	Ala	Ser	Ala	Gly	His	Ala	Val	Ser	Ile	Thr	Gln	Asp	Asp
1					5					10				15	

Gly Gly Ala Asp Asp Trp Glu Thr Asp Pro Asp Phe Val Asn Asp Val
 20 25 30

Ser Glu Lys Glu Gln Arg Trp Gly Ala Lys Thr Val Gln Gly Ser Gly
 35 40 45

His Gln Glu His Ile Asn Ile His Lys Leu Arg Glu Asn Val Phe Gln
 50 55 60

Glu His Gln Thr Leu Lys Glu Lys Glu Leu Glu Thr Gly Pro Lys Ala
 65 70 75 80

Ser His Gly Tyr Gly Gly Lys Phe Gly Val Glu Gln Asp Arg Met Asp
 85 90 95

Arg Ser Ala Val Gly His Glu Tyr Gln Ser Lys Leu Ser Lys His Cys
 100 105 110

Ser Gln Val Asp Ser Val Arg Gly Phe Gly Gly Lys Phe Gly Val Gln
 115 120 125

Met Asp Arg Val Asp Gln Ser Ala Val Gly Phe Glu Tyr Gln Gly Lys
 130 135 140

Thr Glu Lys His Ala Ser Gln Lys Asp Tyr Ser Ser Gly Phe Gly Gly
 145 150 155 160

Lys Tyr Gly Val Gln Ala Asp Arg Val Asp Lys Ser Ala Val Gly Phe
 165 170 175

Asp Tyr Gln Gly Lys Thr Glu Lys His Glu Ser Gln Lys Asp Tyr Ser
 180 185 190

Lys Gly Phe Gly Gly Lys Tyr Gly Ile Asp Lys Asp Lys Val Asp Lys
 195 200 205

Ser Ala Val Gly Phe Glu Tyr Gln Gly Lys Thr Glu Lys His Glu Ser
 210 215 220

Gln Lys Asp Tyr Val Lys Gly Phe Gly Gly Lys Phe Gly Val Gln Thr
 225 230 235 240

Asp Arg Gln Asp Lys Cys Ala Leu Gly Trp Asp His Gln Glu Lys Leu
 245 250 255

Gln Leu His Glu Ser Gln Lys Asp Tyr Lys Thr Gly Phe Gly Gly Lys
 260 265 270

Phe Gly Val Gln Ser Glu Arg Gln Asp Ser Ser Ala Val Gly Phe Asp
 275 280 285

Tyr Lys Glu Arg Leu Ala Lys His Glu Pro Gln Gln Asp Tyr Ala Lys
 290 295 300

Gly Phe Gly Gly Lys Tyr Gly Val Gln Lys Asp Arg Met Asp Lys Asn
 305 310 315 320

Ala Ser Thr Phe Glu Glu Val Val Gln Val Pro Ser Ala Tyr Gln Lys
 325 330 335

Thr Val Pro Ile Glu Ala Val Thr Ser Lys Thr Ser Asn Ile Arg Ala
 340 345 350

Asn Phe Glu Asn Leu Ala Lys Glu Arg Glu Gln Glu Asp Arg Arg Lys
 355 360 365

Ala Glu Ala Glu Arg Ala Gln Arg Met Ala Lys Glu Arg Gln Glu Gln

370

375

380

Glu	Glu	Ala	Arg	Arg	Lys	Leu	Glu	Glu	Gln	Ala	Arg	Ala	Lys	Lys	Gln
385					390				395				400		
Thr	Pro	Pro	Ala	Ser	Pro	Ser	Pro	Gln	Pro	Ile	Glu	Asp	Arg	Pro	Pro
					405				410				415		
Ser	Ser	Pro	Ile	Tyr	Glu	Asp	Ala	Ala	Pro	Phe	Lys	Ala	Glu	Pro	Ser
					420				425				430		
Tyr	Arg	Gly	Ser	Glu	Pro	Glu	Pro	Glu	Tyr	Ser	Ile	Glu	Ala	Ala	Gly
					435				440				445		
Ile	Pro	Glu	Ala	Gly	Ser	Gln	Gln	Gly	Leu	Thr	Tyr	Thr	Ser	Glu	Pro
					450				455				460		
Val	Tyr	Glu	Thr	Thr	Glu	Ala	Pro	Gly	His	Tyr	Gln	Ala	Glu	Asp	Asp
					465				470				475		
Thr	Tyr	Asp	Gly	Tyr	Glu	Ser	Asp	Leu	Gly	Ile	Thr	Ala	Ile	Ala	Leu
					485				490				495		
Tyr	Asp	Tyr	Gln	Ala	Ala	Gly	Asp	Asp	Glu	Ile	Ser	Phe	Asp	Pro	Asp
					500				505				510		
Asp	Ile	Ile	Thr	Asn	Ile	Glu	Met	Ile	Asp	Asp	Gly	Trp	Trp	Arg	Gly
					515				520				525		
Val	Cys	Lys	Gly	Arg	Tyr	Gly	Leu	Phe	Pro	Ala	Asn	Tyr	Val	Glu	Leu
					530				535				540		
Arg	Gln														
	545														

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1199 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAGCAGTCCT	TCACCATGGT	GGCCGACACT	CCGGAAAACC	TCCGCCTCAA	GCAACAGAGC	60
GAGCTGCAGA	GTCAGGTGCG	CTACAAGGAG	GAGTTTGAGA	AGAATAAGGG	CAAAGGTTTC	120
AGCGTGGTGG	CAGACACGCC	TGAGCTGCAG	AGAACATCAAGA	AGACCCAGGA	CCAGATCAGC	180
AATATCAAAT	ACCATGAGGA	GTGGAGAAG	AGCCGCATGG	GGCCCAGTGG	AGGAGAAGGG	240
GTGGAACCAG	AGCGCCGAGA	AGCCCAGGAC	AGCAGCAGCT	ACCGGAGGCC	CACAGAGCAG	300
CAGCAGCCGC	AGCCTCACCA	TATCCCGACC	AGTGCCCCCG	TGTACCAGCA	GCCCCAGCAG	360
CAGCAGATGA	CCTCGTCCTA	TGGTGGGTAC	AAGGAGCCAG	CAGCCCTGT	CTCCATACAG	420
CCGAGTGCC	CAGGTGGCGG	TGGGAAACGG	TACCGTGCAG	TGTATGACTA	CAGCGCTGCC	480
GACGAGGACG	AGGTCTCCTT	CCAGGATGGG	GACACCATCG	TCAATGTGCA	CCAGATCGAT	540
GACGGCTGGA	TGTACGGGAC	CGTAGAGCGC	ACCGGTGACA	CGGGGATGCT	GCCAGCCAAC	600

TACGTGGAGG CCATCTGAAC CCTGTGCCGC CCCGCCCTGT CTTCAATGCA TTCCATGGCA	660
TCACATCTGT CCTGGGGCCT GACCCGTCCA CCCTTCAGTG TCTCTGTCTT TTAAGATCTT	720
CAACTGCTTC TTTATCCCCG CCCCTCCAGC TTATTTTACCC ATCCCAAGCC TTGTTCTGCC	780
CCTGTATGG GCTCCTTCCT CTGGCAGGTT TTCCCTTGGA CCAATCAACT GATTGATTT	840
TCTCTCTGGA TGGAACACAGGC TGGGCACTCT GGGGAGGGCA GGATTGTTCT TAGCTAGGTA	900
GACTCCCAGG GCTGGGCTGA ACTAGGAGAC CCACTAAGGA GATCAGTTA GACTGGGTGC	960
AGTGGCAAAC ACCCTTAATT CCCAGCGAAG GGAGTCAGAG GCAGGCAGAT CTGTGACTTG	1020
GAAGCCAGCC TGGTCTACAT CGAGAGTTTC AGGACAGCCA GAGCTATGTA GTGAGGCCCT	1080
GTCTCGGAGG AAGAGTGGGG GTTGGTTAGC TCTCAGCTTC ACTTCCTGCC TTAGGCTCCT	1140
CAGAACCCCT GGCCCAGCTC CCCCAACTCC CTTCCCTCTA GAGGTGGGGT GAGCTGTGC	1199

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Lys	Gln	Ser	Phe	Thr	Met	Val	Ala	Asp	Thr	Pro	Glu	Asn	Leu	Arg	Leu
1					5				10				15		
Lys	Gln	Gln	Ser	Glu	Leu	Gln	Ser	Gln	Val	Arg	Tyr	Lys	Glu	Glu	Phe
					20			25				30			
Glu	Lys	Asn	Lys	Gly	Lys	Gly	Phe	Ser	Val	Val	Ala	Asp	Thr	Pro	Glu
					35		40				45				
Leu	Gln	Arg	Ile	Lys	Lys	Thr	Gln	Asp	Gln	Ile	Ser	Asn	Ile	Lys	Tyr
					50		55			60					
His	Glu	Glu	Phe	Glu	Lys	Ser	Arg	Met	Gly	Pro	Ser	Gly	Glu	Gly	
					65		70		75			80			
Val	Glu	Pro	Glu	Arg	Arg	Glu	Ala	Gln	Asp	Ser	Ser	Ser	Tyr	Arg	Arg
					85			90				95			
Pro	Thr	Glu	Gln	Gln	Gln	Pro	Gln	Pro	His	His	Ile	Pro	Thr	Ser	Ala
					100			105			110				
Pro	Val	Tyr	Gln	Gln	Pro	Gln	Gln	Gln	Met	Thr	Ser	Ser	Tyr	Gly	
					115			120			125				
Gly	Tyr	Lys	Glu	Pro	Ala	Ala	Pro	Val	Ser	Ile	Gln	Arg	Ser	Ala	Pro
					130			135			140				
Gly	Gly	Gly	Gly	Lys	Arg	Tyr	Arg	Ala	Val	Tyr	Asp	Tyr	Ser	Ala	Ala
					145			150			155			160	
Asp	Glu	Asp	Glu	Val	Ser	Phe	Gln	Asp	Gly	Asp	Thr	Ile	Val	Asn	Val
					165				170			175			
Gln	Gln	Ile	Asp	Asp	Gly	Trp	Met	Tyr	Gly	Thr	Val	Glu	Arg	Thr	Gly

180

185

190

Asp Thr Gly Met Leu Pro Ala Asn Tyr Val Glu Ala Ile	200	205
195		

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1302 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGGCCGGTGA	ACCTGAGCCG	GAACGGGCCG	GCGCTGCAGG	AGGCCTACGT	GCGCGTAGTC	60
ACCGAGAAAT	CCCCGACCGA	CTGGGCTCTT	TTTACCTATG	AAGGCAACAG	CAATGACATC	120
CGTGTGGCTG	GCACAGGAGA	GGGAGGCCTG	GAGGAGCTGG	TGGAAGAGCT	CAACAGCGGG	180
AAGGTGATGT	ACGCCTTCTG	CAGGGTGAAG	GACCCCAACT	CCGGCCTGCC	CAAGTTGTC	240
CTCATCAACT	GGACAGGAGA	GGGTGTGAAT	GATGTGCGGA	AAGGAGCATG	TGCCAACAC	300
GTCAGCACCA	TGGCCAACTT	CCTGAAGGGT	GCCCACGTGA	CCATCAATGC	CCGGGCCGAG	360
GAGGATGTGG	AGCCTGAGTG	CATCATGGAG	AAGGTTGCCA	AGGCCTCTGG	GGCCAACCTAC	420
AGCTTCCATA	AGGAAAGCAC	CTCCTTCCAG	GATGTAGGGC	CGCAGGCCCC	AGTGGGCTCT	480
GTGTACCAGA	AGACCAATGC	CATATCTGAG	ATCAAGAGAG	TCGGCAAGGA	TAACTTCTGG	540
GCCAAAGCTG	AGAAGGAAGA	AGAGAACCGC	CGCCTGGAGG	AGAAGCGCG	TGCCGAAGAG	600
GAGCGGCAGC	GGTTGGAGGA	GGAGCGACGA	GAGCGGGAGC	TGCAGGAGGC	TGCCCGACGT	660
GAGCAGCGCT	ACCAAGAACCA	GCACAGATCA	GCTGGAGCCC	CGAGCAGGAC	AGGTGAGCCA	720
GAGCAGGAAG	CCGTTCAAG	GACCAGACAG	GAGTGGGAGT	CTGCTGGCA	GCAGGCCCA	780
CACCCACGAG	AGATTTCAA	GCAGAAGGAA	AGGGCAATGT	CCACCACCTC	TGTCACCAGC	840
TCGCAGCCGG	GCAAGCTGAG	GAGCCCCTTC	CTGCAGAACG	AACTCACTCA	ACCAGAAACC	900
TCCTACGGCC	GAGAGCCCAC	AGCTCCTGTC	TCCCCGCTG	CAGCAGGTGT	CTGTGAGGAG	960
CCAGCGCCTA	GCACTCTGTC	TTCTGCCAG	ACAGAAGAAG	AACCTACATA	TGAAGTACCC	1020
CCAGAGCAGG	ACACCCCTCA	TGAGGAACCA	CCACTGGTAC	AGCAGCAAGG	GGCTGGCTCC	1080
GAACACATTG	ACAACATACAT	GCAGAGCCAG	GGCTTCAGTG	GACAAGGGCT	GTGCGCCCGG	1140
GCCTTGTATG	ACTACCAGGC	AGCTGATGAC	ACCGAGATCT	CCTTGACCC	TGAGAACCTA	1200
ATCACAGGCA	TCGAGGTGAT	TGACGAAGGC	TGGTGGCGAG	GCTATGGGCC	TGACGGCCAC	1260
TTTGGCATGT	TTCTGCCAA	CTACGTGGAG	CTCATAGAGT	GA		1302

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Ala Val Asn Leu Ser Arg Asn Gly Pro Ala Leu Gln Glu Ala Tyr
 1 5 10 15

Val Arg Val Val Thr Glu Lys Ser Pro Thr Asp Trp Ala Leu Phe Thr
 20 25 30

Tyr Glu Gly Asn Ser Asn Asp Ile Arg Val Ala Gly Thr Gly Glu Gly
 35 40 45

Gly Leu Glu Glu Leu Val Glu Glu Leu Asn Ser Gly Lys Val Met Tyr
 50 55 60

Ala Phe Cys Arg Val Lys Asp Pro Asn Ser Gly Leu Pro Lys Phe Val
 65 70 75 80

Leu Ile Asn Trp Thr Gly Glu Gly Val Asn Asp Val Arg Lys Gly Ala
 85 90 95

Cys Ala Asn His Val Ser Thr Met Ala Asn Phe Leu Lys Gly Ala His
 100 105 110

Val Thr Ile Asn Ala Arg Ala Glu Glu Asp Val Glu Pro Glu Cys Ile
 115 120 125

Met Glu Lys Val Ala Lys Ala Ser Gly Ala Asn Tyr Ser Phe His Lys
 130 135 140

Glu Ser Thr Ser Phe Gln Asp Val Gly Pro Gln Ala Pro Val Gly Ser
 145 150 155 160

Val Tyr Gln Lys Thr Asn Ala Ile Ser Glu Ile Lys Arg Val Gly Lys
 165 170 175

Asp Asn Phe Trp Ala Lys Ala Glu Lys Glu Glu Asn Arg Arg Leu
 180 185 190

Glu Glu Lys Arg Arg Ala Glu Glu Glu Arg Gln Arg Leu Glu Glu Glu
 195 200 205

Arg Arg Glu Arg Glu Leu Gln Glu Ala Ala Arg Arg Glu Gln Arg Tyr
 210 215 220

Gln Glu Gln His Arg Ser Ala Gly Ala Pro Ser Arg Thr Gly Glu Pro
 225 230 235 240

Glu Gln Glu Ala Val Ser Arg Thr Arg Gln Glu Trp Glu Ser Ala Gly
 245 250 255

Gln Gln Ala Pro His Pro Arg Glu Ile Phe Lys Gln Lys Glu Arg Ala
 260 265 270

Met Ser Thr Thr Ser Val Thr Ser Ser Gln Pro Gly Lys Leu Arg Ser
 275 280 285

Pro Phe Leu Gln Lys Gln Leu Thr Gln Pro Glu Thr Ser Tyr Gly Arg
 290 295 300

Glu Pro Thr Ala Pro Val Ser Arg Pro Ala Ala Gly Val Cys Glu Glu
 305 310 315 320

Pro Ala Pro Ser Thr Leu Ser Ser Ala Gln Thr Glu Glu Glu Pro Thr
 325 330 335
 Tyr Glu Val Pro Pro Glu Gln Asp Thr Leu Tyr Glu Glu Pro Pro Leu
 340 345 350
 Val Gln Gln Gln Gly Ala Gly Ser Glu His Ile Asp Asn Tyr Met Gln
 355 360 365
 Ser Gln Gly Phe Ser Gly Gln Gly Leu Cys Ala Arg Ala Leu Tyr Asp
 370 375 380
 Tyr Gln Ala Ala Asp Asp Thr Glu Ile Ser Phe Asp Pro Glu Asn Leu
 385 390 395 400
 Ile Thr Gly Ile Glu Val Ile Asp Glu Gly Trp Trp Arg Gly Tyr Gly
 405 410 415
 Pro Asp Gly His Phe Gly Met Phe Pro Ala Asn Tyr Val Glu Leu Ile
 420 425 430
 Glu

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2074 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TTNNCACTCA CCGTCCGTGG TNNNNSTMMC SGWYNKRNTK YRRKMSSKRW YKWKKCRRKS	60
GCGGCGCCGA CCTGCCGCG GAGGAAAGAA GTCGGTTCGG CGGCGCCGGC GGAAACCGGA	120
GTTCGAGCGG GAGGCCTGAC GGCGGCAGGC GGCATGTCGG TGGCGGGGCT GAAGAAGCAG	180
TTCTACAAGG CGAGCCAGCT GGTCAGCGAG AAGGTTGGTG GGGCCGAAGG GACCAAACGTG	240
GATGATGACT TTAAAGATAT GGAAAAGAAG GTGGATGTCA CCAGCAAGGC CGTGGCAGAG	300
GTGCTGGTCA GAACCATAAGA ATATCTGCAG CCTAACCCAG CCTCGAGAGC CAAGCTGACT	360
ATGCTGAACA CCGTATCCAA GATCCGGGGC CAAGTGAAGA ACCCTGGCTA CCCACAGTCA	420
GAGGGTCTGT TGGGAGAGTG CATGGTTCGC CATGGCAAGG AACTAGGTGG AGAGTCCAAC	480
TTCGGTGATG CCCTGCTAGA TGCAGGTGAG TCCATGAAGC GCCTGGCTGA GGTGAAGGAC	540
TCACTGGACA TCGAGGTCAA GCAGAACTTC ATTGACCCAC TACAGAACCT GTGTGACAAG	600
GATCTGAAGG AGATCCAGCA CCACCTGAAG AAATTGGAGG GCCGCCGCCT TGACTTTGAC	660
TACAAGAAGA AGCGCCAGGG CAAGATCCCC GATGAGGAGC TGCAGCCAGGC CCTAGAGAAG	720
TTCGAGGAGT CCAAGGAGGT GGCGGAGACC AGTATGCACA ACCTCCTGGA GACTGATATA	780
GAGCAGGTGA GCCAGCTCTC GCCCCTGGTG GATGCCAGC TGGACTACCA CGGGCAGGCA	840
GTGCAGATCC TGGAGGAGCT GGCTGACAAG CTGAAGCGCA GGGTTCGGGA AGCCTCCTCA	900
CGCCCCAAGC GGGAGTTCAA GCCCCGGCCC CGGGAGCCCT TTGAGCTTGG AGAGCTGGAG	960

CAGCCCAATG	GGGGATTCCC	CTGTCCCCA	GCACCTAAGA	TCACAGCCTC	CTCATCATT	1020
AGATCGTCAG	ACAAGCCCAT	CAGGATGCC	AGCAAGAGCA	TGCCACCCCT	GGACCAGCCA	1080
AGCTGCAAGG	CGCTTATGA	TTTGAGCCA	GAGAATGATG	GCGAGCTGGG	CTTCCGTGAG	1140
GGGGACCTCA	TCACGCTTAC	CAACCGAGTC	GACGAGAACT	GGTATGAGGG	GATGCTGCAC	1200
GGCCAATCAG	GCTTCTTCCC	ACTCAGCTAC	GTGCAGGTGC	TGGTGCCTCT	GCCTCAGTGA	1260
CTGGGCCTT	ACACCGCTGC	CAGTCACAGT	GCAGCAGCAG	TCTAATGCCA	AGGTGCTCTA	1320
GAAACACTAA	TGTTCCTCCA	GGGGGGACTC	CTCCCCACTC	CCTCAGCCCT	GGGGCCCCCC	1380
TATCCTAAGA	CTCGGAAAGG	CCCACCCCTGA	GGTTCTATTG	CCTTCCTGGT	GGTATCAGCT	1440
TCCAGCTGTT	TCAACCCCTTC	CCAGCCCCTT	GCTGGCGATG	GSCCNNGCC	CCCTCTCTAG	1500
GCTCTCTAGA	GGCAGGCAGG	TCCTTGGAAAT	CCCCAGCCTG	CAAGCAGAGG	CTGGCCAGCT	1560
CCCCAGCTCA	GCACACAGAG	ACACCTGGCA	CCTGCTGCTC	ATGAAGAAGT	GCACAAGGCA	1620
CAAATGTGTA	CACTTCCAT	GGGACCACAG	ACCCAGCTCA	GCTCTGTTGA	AGACCAAGCA	1680
CAAAGGCCTT	GAAGAGTGGA	CATTCCCAGG	TCCCTGGCAC	CTTCCCTTGA	GCCAGCTCCA	1740
TTGCTACTTA	TTCATGTGAC	TGAAGCTGAC	CACAGGCAGC	TGGCAGGTCC	TTTTTCAAC	1800
CAGCAGGCTA	GGCTGGCCAT	AGACCCAGCT	CTGCCTCAC	CTGCCATGTT	CCAGTAATGG	1860
AGGCCTCCAG	CCTGGGCTCT	ATTACATTCT	TCTCTACAGC	TGCCCCATAA	CCCGTGGCTT	1920
ATCCCTGGCA	CGTGGGGCCA	CACCCCACGC	CCCCTGGATA	GGCAACACTG	TCCTGCTCCA	1980
GCCTGTGCTG	ANATGAACTG	TACTCCTAAT	TTTTTTTAA	AAAAAAAGTA	TTAAATNTCT	2040
CTTTCTATAT	AAAANAAAGN	TGGCCCTANN	NGGA			2074

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 368 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Ser	Val	Ala	Gly	Leu	Lys	Gln	Phe	Tyr	Lys	Ala	Ser	Gln	Leu
1					5				10				15	

Val	Ser	Glu	Lys	Val	Gly	Cys	Ala	Glu	Gly	Thr	Lys	Leu	Asp	Asp	Asp
				20				25				30			

Phe	Lys	Asp	Met	Glu	Lys	Val	Asp	Val	Thr	Ser	Lys	Ala	Val	Ala
			35				40				45			

Glu	Val	Leu	Val	Arg	Thr	Ile	Glu	Tyr	Leu	Gln	Pro	Asn	Pro	Ala	Ser
	50					55				60					

Arg	Ala	Lys	Leu	Thr	Met	Leu	Asn	Thr	Val	Ser	Lys	Ile	Arg	Gly	Gln
	65				70				75			80			

Val	Lys	Asn	Pro	Gly	Tyr	Pro	Gln	Ser	Glu	Gly	Leu	Leu	Gly	Glu	Cys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85	90	95
Met Val Arg His Gly Lys Glu Leu Gly	Gly Glu Ser Asn Phe Gly Asp	
100 105	110	
Ala Leu Leu Asp Ala Gly Glu Ser Met Lys Arg Leu Ala Glu Val Lys		
115 120	125	
Asp Ser Leu Asp Ile Glu Val Lys Gln Asn Phe Ile Asp Pro Leu Gln		
130 135	140	
Asn Leu Cys Asp Lys Asp Leu Lys Glu Ile Gln His His Leu Lys Lys		
145 150	155	160
Leu Glu Gly Arg Arg Leu Asp Phe Asp Tyr Lys Lys Lys Arg Gln Gly		
165 170	175	
Lys Ile Pro Asp Glu Glu Leu Arg Gln Ala Leu Glu Lys Phe Glu Glu		
180 185	190	
Ser Lys Glu Val Ala Glu Thr Ser Met His Asn Leu Leu Glu Thr Asp		
195 200	205	
Ile Glu Gln Val Ser Gln Leu Ser Ala Leu Val Asp Ala Gln Leu Asp		
210 215	220	
Tyr His Arg Gln Ala Val Gln Ile Leu Glu Glu Leu Ala Asp Lys Leu		
225 230	235	240
Lys Arg Arg Val Arg Glu Ala Ser Ser Arg Pro Lys Arg Glu Phe Lys		
245 250	255	
Pro Arg Pro Arg Glu Pro Phe Glu Leu Gly Glu Leu Glu Gln Pro Asn		
260 265	270	
Gly Gly Phe Pro Cys Ala Pro Ala Pro Lys Ile Thr Ala Ser Ser Ser		
275 280	285	
Phe Arg Ser Ser Asp Lys Pro Ile Arg Met Pro Ser Lys Ser Met Pro		
290 295	300	
Pro Leu Asp Gln Pro Ser Cys Lys Ala Leu Tyr Asp Phe Glu Pro Glu		
305 310	315	320
Asn Asp Gly Glu Leu Gly Phe Arg Glu Gly Asp Leu Ile Thr Leu Thr		
325 330	335	
Asn Gln Ile Asp Glu Asn Trp Tyr Glu Gly Met Leu His Gly Gln Ser		
340 345	350	
Gly Phe Phe Pro Leu Ser Tyr Val Gln Val Leu Val Pro Leu Pro Gln		
355 360	365	

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1531 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCTCACTCGC TCTCCCCGCG CACGCTCCGT CTCCGTCAGT CCCCTGAGCT GTTCTAGTGC	60
GCGGCGTGG A GCCAGGGCTC AGGCTGGTGG AGCGGCCGGG GCTGGAGGCT GGGAGTGC	120
CGCGCACGGC CTCCCCGCG CATTATCCGC GCTCGCTTCG GGCGAGGCCG GCGCCAGGAT	180
GGCAGAGATG GGGAGCAAGG GGGTGACGGC GGGGAAGATC GCCAGCAACG TACAGAAGAA	240
GCTGACCCGA GCGCAGGAGA AGGTCTGCA GAAACTGGGG AAGGCGGACG AGACGAAGGA	300
CGAGCAGTTT GAGCAGTGTG TCCAGAACCT CAATAAGCAG CTGACAGAGG GTACCCGGCT	360
GCAGAACGAT CTTCGCACCT ATCTGCCTTC TGTTAAAGCG ATGCACGAAG CCTCCAAGAA	420
GCTGAGTGAG TGTCTTCAGG AGGTGTACGA GCCCGAGTGG CCTGGCAGGG ATGAAGCAAA	480
CAAGATTGCA GAGAACAAATG ACCTACTCTG GATGGACTAC CACCAGAACG TGGTGGACCA	540
GGCTCTGCTG ACCATGGACA CCTACCTAGG CCAGTTCCCT GATATCAAGT CGCGCATTGC	600
CAAGCGGGGG CGGAAGCTGG TGGACTATGA CAGTGCCCGG CACCACTATG AGTCTCTTCA	660
AACCGCCAAA AAGAAGGATG AAGCCAAAAT TGCCAAGGCA GAAGAGGAGC TCATCAAAGC	720
CCAGAACGGTG TTCGAGGAGA TGAACGTGGA TCTGCAGGAG GAGCTGCCAT CCCTGTGGAA	780
CAGCCGTGTA GGTTTCTATG TCAACACGTT CCAGAGCATE CGGGGTCTGG AGGAAAACCTT	840
CCATAAAGAG ATGAGTAAGC TCAATCAGAA CCTCAATGAT GTCCTGGTCA GCCTAGAGAA	900
GCAGCACGGG AGCAACACCT TCACAGTCAA GGCCCAACCC AGTGACAATG CCCCTGAGAA	960
AGGGAACAAAG AGCCCGTCAC CTCCTCCAGA TGGCTCCCCT GCTGCTACCC CTGAGATCAG	1020
AGTGAACCAT GAGCCAGAGC CGGCCAGTGG GGCCTCACCC GGGGCTACCA TCCCCAAGTC	1080
CCCATCTCAG CCAGCAGAGG CCTCCGAGGT GGTGGGTGGA GCCCAGGAGC CAGGGGAGAC	1140
AGCAGCCAGT GAAGCAACCT CCAGCTCTCT TCCGGCTGTG GTGGTGGAGA CCTTCTCCGC	1200
AACTGTGAAT GGGGCGGTGG AGGGCAGCGC TGGGACTGGA CGCTTGGACC TGCCCCCGGG	1260
ATTCATGTTA AAGGTTCAAG CCCAGCATGA TTACACGGCC ACTGACACTG ATGAGCTGCA	1320
ACTCAAAGCT GGCGATGTGG TGTTGGTGAT TCCTTCCAG AACCCAGAGG AGCAGGATGA	1380
AGGCTGGCTC ATGGGTGTGA AGGAGAGCGA CTGGAATCAG CACAAGGAAC TGGAGAAATG	1440
CCGGCGCGTC TTCCCCGAGA ATTTTACAGA GCGGGTACAG TGACGGAGGA GCCTTCCGGA	1500
GTGTGAAGAA CCTTTCCCCC AAAGATGTGT G	1531

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met	Ala	Glu	Met	Gly	Ser	Lys	Gly	Val	Thr	Ala	Gly	Lys	Ile	Ala	Ser
1															
														10	15

Asn Val Gln Lys Lys Leu Thr Arg Ala Gln Glu Lys Val Leu Gln Lys
 20 25 30
 Leu Gly Lys Ala Asp Glu Thr Lys Asp Glu Gln Phe Glu Gln Cys Val
 35 40 45
 Gln Asn Phe Asn Lys Gln Leu Thr Glu Gly Thr Arg Leu Gln Lys Asp
 50 55 60
 Leu Arg Thr Tyr Leu Ala Ser Val Lys Ala Met His Glu Ala Ser Lys
 65 70 75 80
 Lys Leu Ser Glu Cys Leu Gln Glu Val Tyr Glu Pro Glu Trp Pro Gly
 85 90 95
 Arg Asp Glu Ala Asn Lys Ile Ala Glu Asn Asn Asp Leu Leu Trp Met
 100 105 110
 Asp Tyr His Gln Lys Leu Val Asp Gln Ala Leu Leu Thr Met Asp Thr
 115 120 125
 Tyr Leu Gly Gln Phe Pro Asp Ile Lys Ser Arg Ile Ala Lys Arg Gly
 130 135 140
 Arg Lys Leu Val Asp Tyr Asp Ser Ala Arg His His Tyr Glu Ser Leu
 145 150 155 160
 Gln Thr Ala Lys Lys Lys Asp Glu Ala Lys Ile Ala Lys Ala Glu Glu
 165 170 175
 Glu Leu Ile Lys Ala Gln Lys Val Phe Glu Glu Met Asn Val Asp Leu
 180 185 190
 Gln Glu Glu Leu Pro Ser Leu Trp Asn Ser Arg Val Gly Phe Tyr Val
 195 200 205
 Asn Thr Phe Gln Ser Ile Ala Gly Leu Glu Glu Asn Phe His Lys Glu
 210 215 220
 Met Ser Lys Leu Asn Gln Asn Leu Asn Asp Val Leu Val Ser Leu Glu
 225 230 235 240
 Lys Gln His Gly Ser Asn Thr Phe Thr Val Lys Ala Gln Pro Ser Asp
 245 250 255
 Asn Ala Pro Glu Lys Gly Asn Lys Ser Pro Ser Pro Pro Asp Gly
 260 265 270
 Ser Pro Ala Ala Thr Pro Glu Ile Arg Val Asn His Glu Pro Glu Pro
 275 280 285
 Ala Ser Gly Ala Ser Pro Gly Ala Thr Ile Pro Lys Ser Pro Ser Gln
 290 295 300
 Pro Ala Glu Ala Ser Glu Val Val Gly Gly Ala Gln Glu Pro Gly Glu
 305 310 315 320
 Thr Ala Ala Ser Glu Ala Thr Ser Ser Ser Leu Pro Ala Val Val Val
 325 330 335
 Glu Thr Phe Ser Ala Thr Val Asn Gly Ala Val Glu Gly Ser Ala Gly
 340 345 350
 Thr Gly Arg Leu Asp Leu Pro Pro Gly Phe Met Phe Lys Val Gln Ala
 355 360 365
 Gln His Asp Tyr Thr Ala Thr Asp Thr Asp Glu Leu Gln Leu Lys Ala

370	375	380
Gly Asp Val Val Leu Val Ile Pro Phe Gln Asn Pro Glu Glu Gln Asp		
385	390	395
Glu Gly Trp Leu Met Gly Val Lys Glu Ser Asp Trp Asn Gln His Lys		
405	410	415
Glu Leu Glu Lys Cys Arg Gly Val Phe Pro Glu Asn Phe Thr Glu Arg		
420	425	430
Val Gln		

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1734 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAATTCTCG ACCCACGCGT CCGGTTGAG CAGTGCCTCC AGAATTCAA CAAGCAGCTG	60
ACGGAGGGCA CCCGGCTGCA GAAGGATCTC CGGACCTACC TGGCCTCCGT CAAAGCCATG	120
CACGAGGCTT CCAAGAAGCT GAATGAGTGT CTGCAGGAGG TGTATGAGCC CGATTGGCCC	180
GGCAGGGATG AGGAAACAA GATCGCAGAG AACAAACGACC TGCTGTGGAT GGATTACAC	240
CAGAAGCTGG TGGACCAGGC GCTGCTGACC ATGGACACGT ACCTGGCCA GTTCCCCGAC	300
ATCAAGTCAC GCATTGCCAA GCGGGGGCGC AAGCTGGTGG ACTACGACAG TGCCCGGCAC	360
CACTACGAGT CCCTTCAAAC TGCCAAAAAG AAGGATGAAG CAAAATTGC CAAGGCCGAG	420
GAGGAGCTCA TCAAAGCCC AAGGGTGTGTT GAGGAGATGA ATGTGGATCT GCAGGAGGAG	480
CTGCCGTCCC TGTGGAACAG CCGCGTAGGT TTCTACGTCA ACACGTTCCA GAGCATCGCG	540
GGCCTGGAGG AAAACTTCCA CAAGGAGATG AGCAAGCTCA ACCAGAACCT CAATGATGTG	600
CTGGTCGGCC TGGAGAAGCA ACACGGGAGC AACACCTCCA CGGTCAAGGC CCAGCCCAGT	660
GACAACGCGC CTGCAAAGG GAACAAAGAGC CCTTCGCCTC CAGATGGCTC CCCTGCCGCC	720
ACCCCCGAGA TCAGAGTCAA CCACGAGCCA GAGCCGGCCG GCGGGGCCAC GCCCGGGGCC	780
ACCCCTCCCCA AGTCCCCATC TCAGCCAGCA GAGGCCTCGG AGGTGGCGGG TGGGACCCAA	840
CCTGCGGCTG GAGCCCAGGA GCCAGGGAG ACGGCGGCAA GTGAAGCAGC CTCCAGCTCT	900
CTTCCTGCTG TCGTGGTGG A GACCTTCCA GCAACTGTGA ATGGCACCGT GGAGGGCGGC	960
AGTGGGGCCG GGCGCTTGG A CCTGCCCCCA GGTTTCATGT TCAAGGTACA GGCCCAGCAC	1020
GAATACACGG CCACTGACAC AGACGAGCTG CAGCTCAAGG CTGGTGATGT GGTGCTGGTG	1080
ATCCCCCTCC AGAACCTGA AGAGCAGGAT GAAGGCTGGC TCATGGCGT GAAGGAGAGC	1140
GAATGGAACC AGCACAAGGA GCTGGAGAAG TGCCGTGGCG TCTTCCCCGA GAACTTCACT	1200

GAGAGGGTCC CATGACGGCG GGGCCCAGGC AGCCTCCGGG CGTGTGAAGA ACACCTCCTC	1260
CCGAAAAATG TGTGGTTCTT TTTTTGTTT TGTTTCGTT TTTCATCTT TGAAGAGCAA	1320
AGGGAAATCA AGAGGAGACC CCCAGGCAGA GGGGCCTCT CCCAAAGATT AGGTCGTTTT	1380
CCAAAGAGCC GCGTCCCGGC AAGTCCGGCG GAATTACCCA GTGTCCCTGAA GCTGCTGTGT	1440
CCTCTAGTTG AGTTCTGGCG CCCCTGCCTG TGCCCGCATG TGTGCCTGGC CGCAGGGCGG	1500
GGCTGGGGC TGCCGAGCCA CCATGCTTGC CTGAAGCTTC GGCCGCGCCA CCCGGGCAAG	1560
GGTCCTCTTT TCCTGGCAGC TGCTGTGGGT GGGGCCCAGA CACCAGCCTA ACCTGGCTCT	1620
GCCCCGCAGA CGGTCTGTGT GCTGTTGAA AATAAATCTT AGTGTCAAA ACAAAATGAA	1680
ACAAAAAAA TGATAAAAAA AAAAAAAA AAAAGGGCGG CCGC	1734

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 404 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Glu Phe Val Asp Pro Arg Val Arg Phe Glu Gln Cys Val Gln Asn Phe	
1 5 10 15	
Asn Lys Gln Leu Thr Glu Gly Thr Arg Leu Gln Lys Asp Leu Arg Thr	
20 25 30	
Tyr Leu Ala Ser Val Lys Ala Met His Glu Ala Ser Lys Lys Leu Asn	
35 40 45	
Glu Cys Leu Gln Glu Val Tyr Glu Pro Asp Trp Pro Gly Arg Asp Glu	
50 55 60	
Ala Asn Lys Ile Ala Glu Asn Asn Asp Leu Leu Trp Met Asp Tyr His	
65 70 75 80	
Gln Lys Leu Val Asp Gln Ala Leu Leu Thr Met Asp Thr Tyr Leu Gly	
85 90 95	
Gln Phe Pro Asp Ile Lys Ser Arg Ile Ala Lys Arg Gly Arg Lys Leu	
100 105 110	
Val Asp Tyr Asp Ser Ala Arg His His Tyr Glu Ser Leu Gln Thr Ala	
115 120 125	
Lys Lys Lys Asp Glu Ala Lys Ile Ala Lys Ala Glu Glu Glu Leu Ile	
130 135 140	
Lys Ala Gln Lys Val Phe Glu Glu Met Asn Val Asp Leu Gln Glu Glu	
145 150 155 160	
Leu Pro Ser Leu Trp Asn Ser Arg Val Gly Phe Tyr Val Asn Thr Phe	
165 170 175	
Gln Ser Ile Ala Gly Leu Glu Glu Asn Phe His Lys Glu Met Ser Lys	
180 185 190	

Leu Asn Gln Asn Leu Asn Asp Val Leu Val Gly Leu Glu Lys Gln His
 195 200 205
 Gly Ser Asn Thr Ser Thr Val Lys Ala Gln Pro Ser Asp Asn Ala Pro
 210 215 220
 Ala Lys Gly Asn Lys Ser Pro Ser Pro Pro Asp Gly Ser Pro Ala Ala
 225 230 235 240
 Thr Pro Glu Ile Arg Val Asn His Glu Pro Glu Pro Ala Gly Gly Ala
 245 250 255
 Thr Pro Gly Ala Thr Leu Pro Lys Ser Pro Ser Gln Pro Ala Glu Ala
 260 265 270
 Ser Glu Val Ala Gly Gly Thr Gln Pro Ala Ala Gly Ala Gln Glu Pro
 275 280 285
 Gly Glu Thr Ala Ala Ser Glu Ala Ala Ser Ser Ser Leu Pro Ala Val
 290 295 300
 Val Val Glu Thr Phe Pro Ala Thr Val Asn Gly Thr Val Glu Gly Gly
 305 310 315 320
 Ser Gly Ala Gly Arg Leu Asp Leu Pro Pro Gly Phe Met Phe Lys Val
 325 330 335
 Gln Ala Gln His Asp Tyr Thr Ala Thr Asp Thr Asp Glu Leu Gln Leu
 340 345 350
 Lys Ala Gly Asp Val Val Leu Val Ile Pro Phe Gln Asn Pro Glu Glu
 355 360 365
 Gln Asp Glu Gly Trp Leu Met Gly Val Lys Glu Ser Asp Trp Asn Gln
 370 375 380
 His Lys Glu Leu Glu Lys Cys Arg Gly Val Phe Pro Glu Asn Phe Thr
 385 390 395 400
 Glu Arg Val Pro

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2003 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CAGCCGCTGG	AGGGGGCGCC	TGGTGTAGAT	GTGAAAAGCC	GTAACCAGGA	ACCAAGTAAAG	60
ATGTGGAAGT	CTGTAGTGGG	GCATGATGTA	TCGGTTTCCG	TGGAGACCCA	GGGTGATGAC	120
TGGGATACAG	ACCCCTGACTT	TGTGAATGAC	ATCTCCGAGA	AGGAGCAACG	GTGGGGAGCC	180
AAGACCATTG	AGGGCTCTGG	ACGCACAGAG	CACATCAACA	TCCACCAGCT	GAGGAACAAA	240
GTGTCAGAGG	AGCACCGACAT	CCTCAAGAAG	AAGGAGCTGG	AATCGGGGCC	TAAGGCATCC	300
CATGGCTATG	GCGGTCAGTT	TGGAGTGGAG	AGAGACCGGA	TGGACAAGAG	TGCCGTGGGC	360

CACGAGTATG TTGCTGATGT GGAGAACAC TCATCTCAGA CTGATGCSGC CAGAGGCTTT	420
GGGGGCAAAAT ATGGAGTTGA GAGGGACCGG GCAGACAAGT CAGCGGTGGG CTTTGACTAC	480
AAAGGAGAAG TGGAAAAGCA TGCATCTCAG AAAGATTACT CTCATGGCTT TGGTGGCCGC	540
TACGGGGTAG AGAAGGATAA ACGGGACAAA GCAGCCCTGG GATACGACTA CAAAGGAGAG	600
ACGGAGAAGC ACGAGTCTCA GAGAGATTAT GCCAAGGGCT TTGGTGGCCA ATATGGAATC	660
CAGAAAGACC GAGTGGATAA GAGTGCTGTT GGCTTCAATG AAATGGAGGC CCCAACACG	720
CCGTATAAGA ACACAAACACC CATAGAACGCT GCTTCCAGTG GTGCCCGTGG GCTGAAGGCA	780
AAATTTGAGT CCCTGGCTGA GGAGAAGAGG AAGCGAGAGG AAGAAGAGAA GGACACAGCAG	840
ATGGCCAGGC AGCAACAGGA GCGAAAGGCT GTGGTAAAGA TGAGCCGAGA AGTCCAGCAG	900
CCATCCATGC CTGTGGAAGA GCCAGCGGCA CCAGCCCAGT TGCCCAAGAA GATCTCCTCA	960
GAGGTCTGGC CTCCAGCAGA GAGTCACCTA CCGCCAGAGT CTCAGCCAGT GAGAACAGA	1020
AGGGAATACC CTGTGCCCTC TCTGCCACG AGGCAGTCTC CATTGCAGAA TCACTTGGAG	1080
GACAACGAGG AGCCCCCAGC TCTGCCCTC AGGACCCAG AAGGCCTCCA GGTGGTGGAA	1140
GAGCCAGTGT ACGAACGAGC ACCCGAGCTG GAGCCGGAGC CAGAGCCTGA CTATGAGCCA	1200
GAGCCAGAGA CAGAGCCTGA CTATGAGGAT GTTGGGGAGT TAGATCGGCA GGATGAGGAT	1260
GCAGAGGGAG ACTATGAGGA TGTGCTGGAG CCCGANGACA CCCCTTCTCT GTCCTACCAA	1320
GCTGGACCT CAGCTGGGGC TGGTGGTGC GGGATCTCTG CTATAGCCCT GTATGATTAC	1380
CAAGGAGAGG GAAGCGATGA GCTTCCTTT GATCCAGATG ACATCATCAC TGACATTGAG	1440
ATGGTGGATG AAGGCTGGTG GCGGGGCCAA TGCCGTGGCC ACTTTGGACT TTTCCCTGCA	1500
AACTATGTCA AGCTCCTCTA ATGACCAGCC CATTGTCTTC CGACTTCCCG AATTGAAAGC	1560
TGCTCTGCCT CCCTCTTCCC ACTCCATGGT ACTGCTGCAA GGACCTGGCT GAACATCATG	1620
AGATGCCTGA AGTTCTGGCA GTCTGTCTCC CGCCTTTA AGAGCTTTAG GTAGAATCGC	1680
TCCAGGTGGG GGTGGGGGTG GGGGTGGGAT CCCTCTGTCC CTCTGTCACC ACTCTTCCCT	1740
GAGGTAGCTC ATGAAATCAT CTTGCAGACC TGCCCTCTTC AGCCGCACCC CAGCTCTGCC	1800
AACCTTGCTC TAGAGTGCTG GGATTCCTT GCCCCGACCC TGGGTGCCAG CCTAGAGGGG	1860
AGGCTCTCAC AGGGCTGCCT GATTGCCCC GTTGTGCTTT TGCTCATTTC TCTTCCCTTA	1920
GCAGACAAAT TGGAAC TGCC CTTCTGTTA GTCTAAAAC TGAAAATAAA ATGAGACTGT	1980
GGCTAAAAAA AAAAAAAA AAA	2003

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 486 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Trp Lys Ser Val Val Gly His Asp Val Ser Val Ser Val Glu Thr
1 5 10 15

Gln Gly Asp Asp Trp Asp Thr Asp Pro Asp Phe Val Asn Asp Ile Ser
20 25 30

Glu Lys Glu Gln Arg Trp Gly Ala Lys Thr Ile Glu Gly Ser Gly Arg
35 40 45

Thr Glu His Ile Asn Ile His Gln Leu Arg Asn Lys Val Ser Glu Glu
50 55 60

His Asp Ile Leu Lys Lys Glu Leu Glu Ser Gly Pro Lys Ala Ser
65 70 75 80

His Gly Tyr Gly Gly Gln Phe Gly Val Glu Arg Asp Arg Met Asp Lys
85 90 95

Ser Ala Val Gly His Glu Tyr Val Ala Asp Val Glu Lys His Ser Ser
100 105 110

Gln Thr Asp Ala Ala Arg Gly Phe Gly Gly Lys Tyr Gly Val Glu Arg
115 120 125

Asp Arg Ala Asp Lys Ser Ala Val Gly Phe Asp Tyr Lys Gly Glu Val
130 135 140

Glu Lys His Ala Ser Gln Lys Asp Tyr Ser His Gly Phe Gly Gly Arg
145 150 155 160

Tyr Gly Val Glu Lys Asp Lys Arg Asp Lys Ala Ala Leu Gly Tyr Asp
165 170 175

Tyr Lys Gly Glu Thr Glu Lys His Glu Ser Gln Arg Asp Tyr Ala Lys
180 185 190

Gly Phe Gly Gly Gln Tyr Gly Ile Gln Lys Asp Arg Val Asp Lys Ser
195 200 205

Ala Val Gly Phe Asn Glu Met Glu Ala Pro Thr Thr Ala Tyr Lys Lys
210 215 220

Thr Thr Pro Ile Glu Ala Ala Ser Ser Gly Ala Arg Gly Leu Lys Ala
225 230 235 240

Lys Phe Glu Ser Leu Ala Glu Glu Lys Arg Lys Arg Glu Glu Glu
245 250 255

Lys Ala Gln Gln Met Ala Arg Gln Gln Gln Glu Arg Lys Ala Val Val
260 265 270

Lys Met Ser Arg Glu Val Gln Gln Pro Ser Met Pro Val Glu Glu Pro
275 280 285

Ala Ala Pro Ala Gln Leu Pro Lys Lys Ile Ser Ser Glu Val Trp Pro
290 295 300

Pro Ala Glu Ser His Leu Pro Pro Glu Ser Gln Pro Val Arg Ser Arg
305 310 315 320

Arg Glu Tyr Pro Val Pro Ser Leu Pro Thr Arg Gln Ser Pro Leu Gln
325 330 335

Asn His Leu Glu Asp Asn Glu Glu Pro Pro Ala Leu Pro Pro Arg Thr
340 345 350

Pro Glu Gly Leu Gln Val Val Glu Glu Pro Val Tyr Glu Ala Ala Pro
 355 360 365
 Glu Leu Glu Pro Glu Pro Glu Pro Asp Tyr Glu Pro Glu Pro Glu Thr
 370 375 380
 Glu Pro Asp Tyr Glu Asp Val Gly Glu Leu Asp Arg Gln Asp Glu Asp
 385 390 395 400
 Ala Glu Gly Asp Tyr Glu Asp Val Leu Glu Pro Glu Asp Thr Pro Ser
 405 410 415
 Leu Ser Tyr Gln Ala Gly Pro Ser Ala Gly Ala Gly Gly Ala Gly Ile
 420 425 430
 Ser Ala Ile Ala Leu Tyr Asp Tyr Gln Gly Glu Gly Ser Asp Glu Leu
 435 440 445
 Ser Phe Asp Pro Asp Asp Ile Ile Thr Asp Ile Glu Met Val Asp Glu
 450 455 460
 Gly Trp Trp Arg Gly Gln Cys Arg Gly His Phe Gly Leu Phe Pro Ala
 465 470 475 480
 Asn Tyr Val Lys Leu Leu
 485

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGATCCCCGG AGCCGGTCCG CTGGGCGGGG CGCAGGGCTG GAGGGCGCG CGTGCCGGCG	60
GCGGCCAGC GTGAAAGCGC GGAGGCGGCC ATGGCGGGCA ACTTCGACTC GGAGGAGCGG	120
AGTAGCTGGT ACTGGGGCCG CCTGAGCCGG CAGGAGGCGG TGGCGCTATT GCAGGGCCAG	180
CGGCACGGGG TGTTCCCTGGT GCGGGACTCG AGCACCAAGCC CCGGGGACTA TGTGCTTAGC	240
GTCTCCGAAA ACTCGCGCGT CTCCCACTAC ATCATCAACA GCAGGGCCCC GCGCCCTCCA	300
GTGCCTCCGT CGCCCGCTCA GCCTCCGCGG GGAGTGAGTC CCTCCAGCCT CCGAATAGGA	360
GATCAAGAAT TTGATTCAATT GCCTGCTTTA CTGGAATTCT ACAAAATACA CTATTTGGAC	420
ACTACAACAT TGATAGAACCC AGTGGCCAGA TCAAGGCAGG GTAGTGGAGT GATTCTCAGG	480
CAGGAGGAGG CAGAGTATGT GCGGGCCCTG TTTGACTTTA ATGGGAATGA TGAAGAAGAT	540
CTTCCCTTTA AGAAAGGAGA CATCCTGAGA ATCCGGATA AGCCTGAAGA GCAGTGGTGG	600
AATGCAGAGG ACAGCGAAGG AAAGAGGGGG ATGATTCTG TCCCTTACGT GGAGAAGTAT	660
AGACCTGCCT CCGCCCTCAGT ATCGGCTCTG ATTGGAGGTA ACCAGGAGGG TTCCCACCCA	720
CAGCCACTGG GTGGGCCCGGA GCCTGGGCC TATGCCAAC CCAGCGTCAA CACTCCGCTC	780
CCTAACCTCC AGAATGGGCC CATTATGCC AGGGTTATCC AGAAGCGAGT CCCTAACGCC	840

TACGACAAGA CAGCCTTGGC TTTGGAGGTC GGTGAGCTGG TAAAGGTTAC GAAGATTAAT	900
GTGAGTGGTC AGTGGGAAGG GGAGTGTAAAT GGCAAACGAG GTCACTTCCC ATTACACACAT	960
GTCCGTCTGC TGGATCAACA GAATCCCGAT GAGGACTTCA GCTGAGTATA GCTCGACAGT	1020
TTGCTGACAG ATGGAACAAT CTGTTTCCC CCAATTGCCA TCTATACAAT TTTCTTACAG	1080
GTGTCAAAGC AGTCTAGTTT ATATAAGCAT TCTGTTACCT GGGATTTTT TTAAGACTGA	1140
ACTACTCCAT TCTCACTTGT ATTTACCATA TTCAGGGTAC GAAACCGGAG GCCTTATGTG	1200
GTAACTTCT GAGTTGGCAG TTTAGGTGG TAGTGGCCGT GCCTGTATGA GAAGACGTAA	1260
ATACATTGCC TCCTTCTTT TGGGCAAAAC AGATCA	1296

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 304 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Ala Gly Asn Phe Asp Ser Glu Glu Arg Ser Ser Trp Tyr Trp Gly	
1 5 10 15	
Arg Leu Ser Arg Gln Glu Ala Val Ala Leu Leu Gln Gly Gln Arg His	
20 25 30	
Gly Val Phe Leu Val Arg Asp Ser Ser Thr Ser Pro Gly Asp Tyr Val	
35 40 45	
Leu Ser Val Ser Glu Asn Ser Arg Val Ser His Tyr Ile Ile Asn Ser	
50 55 60	
Ser Gly Pro Arg Pro Pro Val Pro Pro Ser Pro Ala Gln Pro Pro Pro	
65 70 75 80	
Gly Val Ser Pro Ser Arg Leu Arg Ile Gly Asp Gln Glu Phe Asp Ser	
85 90 95	
Leu Pro Ala Leu Leu Glu Phe Tyr Lys Ile His Tyr Leu Asp Thr Thr	
100 105 110	
Thr Leu Ile Glu Pro Val Ala Arg Ser Arg Gln Gly Ser Gly Val Ile	
115 120 125	
Leu Arg Gln Glu Glu Ala Glu Tyr Val Arg Ala Leu Phe Asp Phe Asn	
130 135 140	
Gly Asn Asp Glu Glu Asp Leu Pro Phe Lys Lys Gly Asp Ile Leu Arg	
145 150 155 160	
Ile Arg Asp Lys Pro Glu Glu Gln Trp Trp Asn Ala Glu Asp Ser Glu	
165 170 175	
Gly Lys Arg Gly Met Ile Pro Val Pro Tyr Val Glu Lys Tyr Arg Pro	
180 185 190	
Ala Ser Ala Ser Val Ser Ala Leu Ile Gly Gly Asn Gln Glu Gly Ser	
195 200 205	

His Pro Gln Pro Leu Gly Gly Pro Glu Pro Gly Pro Tyr Ala Gln Pro
 210 215 220
 Ser Val Asn Thr Pro Leu Pro Asn Leu Gln Asn Gly Pro Ile Tyr Ala
 225 230 235 240
 Arg Val Ile Gln Lys Arg Val Pro Asn Ala Tyr Asp Lys Thr Ala Leu
 245 250 255
 Ala Leu Glu Val Gly Glu Leu Val Lys Val Thr Lys Ile Asn Val Ser
 260 265 270
 Gly Gln Trp Glu Gly Glu Cys Asn Gly Lys Arg Gly His Phe Pro Phe
 275 280 285
 Thr His Val Arg Leu Leu Asp Gln Gln Asn Pro Asp Glu Asp Phe Ser
 290 295 300

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3345 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCTCACCGNN	CCTGGTGTAG	GTACCGGATC	GAATTCAAGC	AAAAAACAGA	GCGGGGCTGA	60
CTGTAGCGTG	GAGCGCGAGC	CGGGCTGGAC	GCGCGCAAGC	CCTTGCCGGG	GACCCGCGAG	120
GCAAGCAGTC	TCCCTGTGGA	GCGTCGTCCCT	CCATCCCTGT	AAGCACCGTT	ACAGAGAATG	180
AAACAAGGGC	AGAAGTTACA	GAGCCCGTGA	GGCATCTTCA	AATAGAAAGAC	TGGAGACTAG	240
AAAAAGAATA	TTGCCAGGAG	TTGGCATCCA	TTGGAAGACC	TTGAGATCCT	CTCAGCTCAG	300
AACTCCAGGA	CCGATGCATC	TTCCCACCAAC	CTTGAAGCAC	TGAGCCCTCC	AGAGCTGCAT	360
CTGGGAAGAC	TCGCCTGCCT	CCAGCATGAG	TTCTGAATGT	GATGTTGGAA	GCTCTAAAGC	420
TGTGGTGAAT	GGCTTGGCAT	CTGGCAACCA	TGGACCAGAC	AAAGACATGG	ACCCTACCAA	480
AATCTGCACT	GGGAAAGGAA	CAGTGACTCT	TCGGGCCTCG	TCTTCCTACA	GGGAAACCCC	540
AAGCAGCAGC	CCTGTGAGCC	CCCAGGAATC	TCCGAAGCAT	GAAAGCAAGT	CAGATGAATG	600
GAAACTTTCT	TCCAGTGCAG	ATACCAATGG	CAACGCCAG	CCCTCCCCAC	TTGCTGCCAA	660
GGGCTATAGA	AGTGTGCATC	CCAGCCTTTC	TGCTGACAAG	CCCCAGGGCA	GTCCTTTACT	720
AAACGAAGTT	TCTTCTTCCC	ACATTGAAAC	CGATTCCCAA	GACTTCCCTC	CAACAAGCAG	780
ACCTTCGTCT	GCCTACCCCT	CCACCACCAT	CGTCAACCCCT	ACCATTGTGC	TCCTGCAGCA	840
CAATCGAGAG	CAGCAAAAGC	GACTCAGTAG	TCTTCAGAT	CCTGCCTCAG	AGAGAAAGAGC	900
GGGTGAGCAG	GACCCAGTAC	CAACCCCCAGC	AGAACTCACT	TCGCCCCGCA	GGGCTTCTGA	960
GAGAAGGGCA	AAGGATGCTA	GCAGACGGGT	GGTGAGGAGC	GCACAGGACC	TGAGCGATGT	1020
GTCTACAGAT	GAAGTGGGCA	TTCCACTCCG	GAATACCGAG	CGATCGAAAG	ACTGGTACAA	1080

AACTATGTTT	AAACAGATCC	ACAAACTGAA	CAGAGATGAT	GATTCTGATG	TCCATTCCCC	1140
TCGATACTCC	TTCTCTGATG	ACACAAAGTC	TCCCCTTCT	GTGCCTCGCT	CAAAAAGTGA	1200
GATGAACTAC	ATCGAAGGGG	AGAAAGTGGT	TAAGAGGTCC	GCCACACTCC	CCCTCCCAGC	1260
CCGCTCTTCC	TCACTCAAGT	CCAGCCCGA	AAGAAACGAC	TGGGAGCCCC	TAGATAAGAA	1320
AGTGGATACG	AGAAAATACC	GAGCAGAGCC	CAAAGCATT	TACGAATATC	AGCCGGGCAA	1380
GTCTTCGGTC	CTGACCAATG	AGAAGATGAG	TCGGGATATA	AGCCCAGAAG	AGATAGATT	1440
AAAGAATGAA	CCTTGGTATA	AATTCTTTTC	GGAAATTGGAG	TTTGGGAGAC	CGAGCTCAGC	1500
AGTCAGCCCG	ACTCCAGACA	TTACGTCAGA	GCCTCCTGGA	TATATCTATT	CTTCCAACCT	1560
CCATGCAGTG	AAGAGAGAAT	CGGACGGGAC	CCCCGGGGT	CTCGCTAGCT	TGGAGAATGA	1620
GAGGCAGATC	TATAAGAGTG	TCTTGGAAAGG	TGGCGACATC	CCTCTTCAGG	GCCTCAGTGG	1680
GCTCAAGCGA	CCTTCCAGCT	CAGCTTCCAC	TAAAGATTCA	GAGTCACCAA	GACATTTTAT	1740
ACCACTGAT	TACTTGGAGT	CCACAGAAGA	ATTTATTCTGG	AGACGGCACG	ATGATAAAGA	1800
GAAAACTTTA	CGGGACCAGA	GACGACTTAA	GCGCGAGCAA	GAAGAGGCCG	ATATTGCAGC	1860
TCGCCGCCAC	ACAGGTGTCA	TCCCAGCTCA	TCATCAGTT	ATCACTAATG	AGCGCTTTGG	1920
GGACCTCCTC	AATATAGATG	ATACGGCCAA	AAGGAAATCT	GGGTTAGAGA	TGAGACCTGC	1980
TCGAGCCAAA	TTTGACTTTA	AAGCCCAGAC	CCTGAAGGAG	CTGCCTCTGC	AGAAGGGAGA	2040
CGTTGTTTAC	ATCTACAGAC	AGATTGACCA	GAACCTGGTAT	GAAGGTGAAC	ACCATGGCCG	2100
GGTGGGAATC	TTCCCACGCA	CCTATATCGA	GCTTCTTCCT	CCAGCTGAGA	AGGCTCAGCC	2160
CAGAAAGTTG	GCACCCGTAC	AAGTTTGGA	ATATGGAGAA	GCCATTGCAA	AGTTAACTT	2220
TAATGGAGAT	ACACAAAGTAG	AAATGTCTTT	CCGAAAGGGG	GAGAGGATCA	CGCTGCTCCG	2280
ACAGGTGGAT	GAGAACTGGT	ATGAAGGGAG	GATTCTGGG	ACATCTCGCC	AAGGCATTTT	2340
CCCTATCACC	TATGTAGATG	TGCTTAAGAG	GCCATTGGTG	AAAACCCCTG	TGGATTACAT	2400
CGACCTGCCT	TATTCTTCTT	CCCCAAGTCG	CAGTGCCACT	GTGAGCCCAC	AGGCTTCTCA	2460
TCATTCATTG	AGCGCAGGAC	CTGATCTCAC	AGAATCTGAA	AAGAACTATG	TGCAACCTCA	2520
AGCCCAGCAG	CGAAGAGTCA	CCCCAGACAG	GAGTCAGCCC	TCACTGGATT	TGTGTAGCTA	2580
CCAAGCGTTA	TATAGTTATG	TGCCACAGAA	CGATGATGAG	TTGGAACCTCC	GAGATGGAGA	2640
TATTGTTGAT	GTCATGGAAA	AATGTGACGA	TGGATGGTTT	GTTGGCACTT	CGAGAAGGAC	2700
GAGGCAGTTT	GGTACTTTTC	CAGGCAACTA	TGTAAAACCT	TTATATCTAT	AAGAAGACTA	2760
AAAAGCACAG	AGATTATTTT	TTATCGGAGG	ATGAAGCATC	ATTCACTAAC	TGGTCTCTTT	2820
ATTTAAGTAC	TGAGTCAGTA	AGAAAACCAA	TGCAGTTGGT	AAAGAAAGAA	TTCAAAGAAC	2880
GAACAGAGAA	GTGTGTTGA	AACCCATTGT	GTATCAGGGA	TTAACTATCT	GCTGAAGACA	2940
TCTGTATTTA	CATGACTGCT	TCTGGGAGCT	GCTCTAGCCC	CCGCTGCTTG	GGGAATCTGA	3000
TCTGGAGCAT	GTCCATGAGC	AACATTAGCC	AAAAAAAAAA	GCTTGGGCC	TATTCTATAG	3060
TGTCACCTAA	ATACTAGCTT	GATCCGGCTG	CTAACAAAGC	CCGAAAGGAA	GCTGAGTTGC	3120

TGCTGCCACC GCTGAGCAAT AACTAGCATA ACCCCTTGGG GCCTCTAAC	GGGTCTTGAG	3180
GGGTTTTTG GCTGAAAGGA GGAACATATAT CCGGATAACC TGGCGTAATA	GCGAAGAGGC	3240
CCGCACCGAT CGCCCTTCCC AACAGTTGGG CAGCCTGAAT GGCATGGG	CGCGCCCTGT	3300
AGCGGCGCAT TAAGCGCGC GGGTGTGGTG GTTACGCGCA GGGTG		3345

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 788 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Ser Ser Glu Cys Asp Val Gly Ser Ser Lys Ala Val Val Asn Gly			
1	5	10	15
Leu Ala Ser Gly Asn His Gly Pro Asp Lys Asp Met Asp Pro Thr Lys			
20	25	30	
Ile Cys Thr Gly Lys Gly Thr Val Thr Leu Arg Ala Ser Ser Ser Tyr			
35	40	45	
Arg Gly Thr Pro Ser Ser Ser Pro Val Ser Pro Gln Glu Ser Pro Lys			
50	55	60	
His Glu Ser Lys Ser Asp Glu Trp Lys Leu Ser Ser Ser Ala Asp Thr			
65	70	75	80
Asn Gly Asn Ala Gln Pro Ser Pro Leu Ala Ala Lys Gly Tyr Arg Ser			
85	90	95	
Val His Pro Ser Leu Ser Ala Asp Lys Pro Gln Gly Ser Pro Leu Leu			
100	105	110	
Asn Glu Val Ser Ser Ser His Ile Glu Thr Asp Ser Gln Asp Phe Pro			
115	120	125	
Pro Thr Ser Arg Pro Ser Ser Ala Tyr Pro Ser Thr Thr Ile Val Asn			
130	135	140	
Pro Thr Ile Val Leu Leu Gln His Asn Arg Glu Gln Gln Lys Arg Leu			
145	150	155	160
Ser Ser Leu Ser Asp Pro Ala Ser Glu Arg Arg Ala Gly Glu Gln Asp			
165	170	175	
Pro Val Pro Thr Pro Ala Glu Leu Thr Ser Pro Gly Arg Ala Ser Glu			
180	185	190	
Arg Arg Ala Lys Asp Ala Ser Arg Arg Val Val Arg Ser Ala Gln Asp			
195	200	205	
Leu Ser Asp Val Ser Thr Asp Glu Val Gly Ile Pro Leu Arg Asn Thr			
210	215	220	
Glu Arg Ser Lys Asp Trp Tyr Lys Thr Met Phe Lys Gln Ile His Lys			
225	230	235	240
Leu Asn Arg Asp Asp Ser Asp Val His Ser Pro Arg Tyr Ser Phe			

245	250	255
Ser Asp Asp Thr Lys Ser Pro Leu Ser Val Pro Arg Ser Lys Ser Glu		
260 265 270		
Met Asn Tyr Ile Glu Gly Glu Lys Val Val Lys Arg Ser Ala Thr Leu		
275 280 285		
Pro Leu Pro Ala Arg Ser Ser Ser Leu Lys Ser Ser Pro Glu Arg Asn		
290 295 300		
Asp Trp Glu Pro Leu Asp Lys Lys Val Asp Thr Arg Lys Tyr Arg Ala		
305 310 315 320		
Glu Pro Lys Ser Ile Tyr Glu Tyr Gln Pro Gly Lys Ser Ser Val Leu		
325 330 335		
Thr Asn Glu Lys Met Ser Arg Asp Ile Ser Pro Glu Glu Ile Asp Leu		
340 345 350		
Lys Asn Glu Pro Trp Tyr Lys Phe Phe Ser Glu Leu Glu Phe Gly Arg		
355 360 365		
Pro Ser Ser Ala Val Ser Pro Thr Pro Asp Ile Thr Ser Glu Pro Pro		
370 375 380		
Gly Tyr Ile Tyr Ser Ser Asn Phe His Ala Val Lys Arg Glu Ser Asp		
385 390 395 400		
Gly Thr Pro Gly Gly Leu Ala Ser Leu Glu Asn Glu Arg Gln Ile Tyr		
405 410 415		
Lys Ser Val Leu Glu Gly Gly Asp Ile Pro Leu Gln Gly Leu Ser Gly		
420 425 430		
Leu Lys Arg Pro Ser Ser Ala Ser Thr Lys Asp Ser Glu Ser Pro		
435 440 445		
Arg His Phe Ile Pro Ala Asp Tyr Leu Glu Ser Thr Glu Glu Phe Ile		
450 455 460		
Arg Arg Arg His Asp Asp Lys Glu Lys Leu Leu Ala Asp Gln Arg Arg		
465 470 475 480		
Leu Lys Arg Glu Gln Glu Glu Ala Asp Ile Ala Ala Arg Arg His Thr		
485 490 495		
Gly Val Ile Pro Thr His His Gln Phe Ile Thr Asn Glu Arg Phe Gly		
500 505 510		
Asp Leu Leu Asn Ile Asp Asp Thr Ala Lys Arg Lys Ser Gly Leu Glu		
515 520 525		
Met Arg Pro Ala Arg Ala Lys Phe Asp Phe Lys Ala Gln Thr Leu Lys		
530 535 540		
Glu Leu Pro Leu Gln Lys Gly Asp Val Val Tyr Ile Tyr Arg Gln Ile		
545 550 555 560		
Asp Gln Asn Trp Tyr Glu Gly Glu His His Gly Arg Val Gly Ile Phe		
565 570 575		
Pro Arg Thr Tyr Ile Glu Leu Leu Pro Pro Ala Glu Lys Ala Gln Pro		
580 585 590		
Arg Lys Leu Ala Pro Val Gln Val Leu Glu Tyr Gly Glu Ala Ile Ala		
595 600 605		

Lys Phe Asn Phe Asn Gly Asp Thr Gln Val Glu Met Ser Phe Arg Lys
 610 615 620
 Gly Glu Arg Ile Thr Leu Leu Arg Gln Val Asp Glu Asn Trp Tyr Glu
 625 630 635 640
 Gly Arg Ile Pro Gly Thr Ser Arg Gln Gly Ile Phe Pro Ile Thr Tyr
 645 650 655
 Val Asp Val Leu Lys Arg Pro Leu Val Lys Thr Pro Val Asp Tyr Ile
 660 665 670
 Asp Leu Pro Tyr Ser Ser Ser Pro Ser Arg Ser Ala Thr Val Ser Pro
 675 680 685
 Gln Ala Ser His His Ser Leu Ser Ala Gly Pro Asp Leu Thr Glu Ser
 690 695 700
 Glu Lys Asn Tyr Val Gln Pro Gln Ala Gln Gln Arg Arg Val Thr Pro
 705 710 715 720
 Asp Arg Ser Gln Pro Ser Leu Asp Leu Cys Ser Tyr Gln Ala Leu Tyr
 725 730 735
 Ser Tyr Val Pro Gln Asn Asp Asp Glu Leu Glu Leu Arg Asp Gly Asp
 740 745 750
 Ile Val Asp Val Met Glu Lys Cys Asp Asp Gly Trp Phe Val Gly Thr
 755 760 765
 Ser Arg Arg Thr Arg Gln Phe Gly Thr Phe Pro Gly Asn Tyr Val Lys
 770 775 780
 Pro Leu Tyr Leu
 785

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1636 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTNNCACTCA CCGTCCTGGT GATGGTACCG GATCGAATT	60
GGCGCGCGGG GACCGCCCGG GGTGCCGCT CCGCTCAGCG	120
GGAGCCCCGA GACCACCCCC GGGCGGGCGC CCGCCGCGAT	180
AGCAGTTCCA CAAAGCCAGC CAGCTGTTA GTGAAAAAAT	240
AGCTAGATGA AGAATTCTG AACATGGAAA AGAAAATAGA	300
TATCACCAAGT AAAAGCTGTT	360
CAGAAATCCT TTCAAAAGCC ACAGAGTATC TCCAACCCAA	420
TCCAGCATAAGC AGAGCTAAC	480
AGACGGAAGG CTTGCTGGGG GACTGCATGC TGAAGTATGG	540
CAAGGAGCTC GGAGAAGACT	
CTGCTTTGG CAACTCGTTG GTAGATGTTG GTGAGGCCCT	
GAAACTCATG GCTGAGGTGA	

AAGACTCTCT GGATATTAAT GTGAAGCAAA CTTTTATTGA CCCACTGCAG CTACTGCAAG	600
ACAAAGATT AAAGGAGATC GGGCACCAAC TGAGAAAGCT GGAAGGCCGT CGCCTGGATT	660
ATGATTATAA AAAGCGCGG GTAGGTAAGA TCCCCGAGGA AGAAATCAGA CAAGCAGTAG	720
AGAAGTTGA AGAGTCAAAG GAGTTGGCCG AAAGGAGCAT GTTTAATTTT TTAGAAAATG	780
ATGTAGAGCA AGTGAGCCAG CTGGCTGTGT TTGTAGAGGC GGCATTAGAC TATCACAGGC	840
AGTCCACAGA GATCCTCCAG GAGCTGCAGA GCAAGCTGGA GTTGCAGATA TCTCTTGCAT	900
CCAAAGTCCC CAAGCGAGAA TTCATGCCAA AGCCTGTGAA CATGAGTTCC ACCGATGCCA	960
ATGGGGTCGG ACCCAGCTCT TCATCAAAGA CACCAGGTAC TGACACTCCC GCGGACCAGC	1020
CCTGCTGTGCG TGGTCTCTAT GACTTGAGC CAGAAAATGA AGGAGAATTA GGATTTAAAG	1080
AAGGGGACAT CATTACATTA ACCAATCAGA TAGATGAAAA CTGGTATGAA GGGATGCTTC	1140
GTGGGGAATC CGGCTCTTC CCCATTAATT ACGTGGAAGT CATTGTGCCT TTACCTCCGT	1200
AAATGTGTCT TTTGGACCTA ACTTCAGAAC TGAAATGAAT TGGCACCAGT GCTCTCTCAG	1260
TGTGGTGTTC TGTGACANCC TCGCTCTCTG GCCCACTTAA TCACTTTGT ATGTGTGTTT	1320
TCTTTATAAT GTATTTGTA TCAATTTAAT TTGTATAACT GATTCTTTG TCCTAACTCA	1380
TAAAAATAGT TTTCTCTTG TTCTAAAAAG TCATTGGTTA AATGTATTTG CTTCTGTTG	1440
CTAAAACGAG TAAATTGCGC CCATTCGAAT GGCTGGGTA GTCCCTGACT GCAGTGGGAA	1500
CGCACCCCTT GCAGCCATGA AAGCTAAAGG TTTGTTCT GACATTATTG ATGGCCTCTG	1560
GTCTTTCCCT GTTTAAGCT TACCTGTGAA CAGCCCAATA AACNTGACAC ACTGTANAAT	1620
AANAAGGGTG GCCCNA	1636

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met	Ser	Val	Ala	Gly	Leu	Lys	Gln	Phe	His	Lys	Ala	Ser	Gln	Leu	
1				5				10				15			
Phe	Ser	Glu	Lys	Ile	Ser	Gly	Ala	Glu	Gly	Thr	Lys	Leu	Asp	Glu	Glu
		20						25				30			
Phe	Leu	Asn	Met	Glu	Lys	Ile	Asp	Ile	Thr	Ser	Lys	Ala	Val	Ala	
	35					40					45				
Glu	Ile	Leu	Ser	Lys	Ala	Thr	Glu	Tyr	Leu	Gln	Pro	Asn	Pro	Ala	Tyr
	50				55					60					
Arg	Ala	Lys	Leu	Gly	Met	Leu	Asn	Thr	Val	Ser	Lys	Leu	Arg	Gly	Gln
	65				70				75			80			
Val	Lys	Ala	Thr	Gly	Tyr	Pro	Gln	Thr	Glu	Gly	Leu	Leu	Gly	Asp	Cys

85	90	95
Met Leu Lys Tyr Gly Lys Glu Leu Gly Glu Asp Ser Ala Phe Gly Asn		
100	105	110
Ser Leu Val Asp Val Gly Glu Ala Leu Lys Leu Met Ala Glu Val Lys		
115	120	125
Asp Ser Leu Asp Ile Asn Val Lys Gln Thr Phe Ile Asp Pro Leu Gln		
130	135	140
Leu Leu Gln Asp Lys Asp Leu Lys Glu Ile Gly His His Leu Arg Lys		
145	150	155
Leu Glu Gly Arg Arg Leu Asp Tyr Asp Tyr Lys Lys Arg Arg Val Gly		
165	170	175
Lys Ile Pro Glu Glu Glu Ile Arg Gln Ala Val Glu Lys Phe Glu Glu		
180	185	190
Ser Lys Glu Leu Ala Glu Arg Ser Met Phe Asn Phe Leu Glu Asn Asp		
195	200	205
Val Glu Gln Val Ser Gln Leu Ala Val Phe Val Glu Ala Ala Leu Asp		
210	215	220
Tyr His Arg Gln Ser Thr Glu Ile Leu Gln Glu Leu Gln Ser Lys Leu		
225	230	235
Glu Leu Arg Ile Ser Leu Ala Ser Lys Val Pro Lys Arg Glu Phe Met		
245	250	255
Pro Lys Pro Val Asn Met Ser Ser Thr Asp Ala Asn Gly Val Gly Pro		
260	265	270
Ser Ser Ser Lys Thr Pro Gly Thr Asp Thr Pro Ala Asp Gln Pro		
275	280	285
Cys Cys Arg Gly Leu Tyr Asp Phe Glu Pro Glu Asn Glu Gly Glu Leu		
290	295	300
Gly Phe Lys Glu Gly Asp Ile Ile Thr Leu Thr Asn Gln Ile Asp Glu		
305	310	315
Asn Trp Tyr Glu Gly Met Leu Arg Gly Glu Ser Gly Phe Phe Pro Ile		
325	330	335
Asn Tyr Val Glu Val Ile Val Pro Leu Pro Pro		
340	345	

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4091 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGGGCTTGAG GCTGGGCCGC CGCCGCCGCC CGCTTGCCA CCCGCCCCGC TGATGGTGTC	60
CGGTGCTCCG GCGCCCAGGG ACACAGACCG GGAGCAGGAC CACTTCTCTC ACCTCCGGAT	120

CTCTCCTGCT	TCCGCAGCCT	GTGAGCAGCA	GGCCTGCTAA	CTGCAGATCC	ACAACCGCAC	180
AGCTCGCTAC	AGGTGCACCA	TGTCTGGCTC	CTACGATGAG	GCCTCAGAGG	AGATCACAGA	240
TAGCTTCTGG	GAGGTGGGA	ACTACAAGCG	GACGGTGAAG	CGCATCGACG	ATGGGCACCG	300
CCTGTGCAAC	GACCTCATGA	GCTGCGTGA	GGAGCGCGCC	AAGATCGAGA	AGGCATACGC	360
GCAGCAGCTC	ACCGACTGGG	CCAAGCGCTG	GCGCCAGCTC	ATCGAGAAAG	GTCCTCAGTA	420
TGGCAGCCTG	GAGCGGGCGT	GGGGCGCCAT	GATGACAGAA	GCAGATAAGG	TCAGCGAGCT	480
GCACCAGGAG	GTGAAGAACAA	GCCTGCTGAA	TGAGGACCTG	GAGAAAGTCA	AGAACTGGCA	540
GAAGGGATGCC	TATCACAAGC	AGATCATGGG	TGGCTTCAAG	GAGACGAAAG	AGGCCGAGGA	600
TGGCTTCCGA	AAGGCCCAGA	AGCCCTGGC	AAAAAAAGATG	AAGGAGCTAG	AGGCCGCGCAA	660
GAAGGCCTAT	CACTTGGCTT	GTAAGGAGGA	AAGGCTGGCC	ATGACCCGGG	AGATGAACAG	720
TAAGACAGAG	CAGTCGGTCA	CCCCTGAACA	GCAGAAGAAA	CTTGTGGACA	AAGTGGACAA	780
ATGCAGACAG	GATGTGCAA	AGACTCAGGA	GAAGTATGAG	AAGGTCTGG	AAGATGTGGG	840
CAAGACCACA	CCACAGTACA	TGGAGGGCAT	GGAGCAGGTG	TTTGAGCAGT	GCCAGCAGTT	900
TGAGGAGAAG	CGGCTGGTCT	TCCTGAAGGA	AGTCCTGCTG	GATATCAAAC	GGCATCTCAA	960
CCTAGCGGAG	AACAGCAGCT	ACATGCATGT	CTACCGAGAA	CTGGAGCAGG	CCATCCGGGG	1020
GGCCGATGCC	CAGGAGGACC	TCAGGTGGTT	CCGCAGCACC	AGTGGCCCCG	GGATGCCCAT	1080
GAACCTGGCCG	CAGTCGAGG	AGTGGAACCC	AGACCTCCCG	CACACCACTG	CCAAGAAGGA	1140
GAAACAGCCT	AAGAAGGCAG	AGGGGGCCAC	CCTGAGCAAT	GCCACTGGGG	CTGTAGAATC	1200
CACATCCCAG	GCTGGGGACC	GTGGCAGTGT	TAGCAGCTAT	GACCGAGGCC	AAACATATGC	1260
CACCGAGTGG	TCAGACGATG	AGAGCGGAAA	CCCCTCGGG	GGCAATGAGG	CCAATGGTGG	1320
CGCCAACCCC	TTCGAGGATG	ATGCCAAGGG	AGTCGTGTA	CGGGCACTCT	ATGACTACGA	1380
CGGTCAGGAG	CAGGATGAGC	TCAGCTCAA	GGCCGGAGAT	GAGCTCACCA	AGCTCGGAGA	1440
GGAAGACGAA	CAGGGTTGGT	GCCGCGGGCG	GCTGGACAGC	GGACAGCTGG	GCCTCTATCC	1500
TGCCAACTAC	GTTGAGGCTA	TATAGCTACC	TTGCCACCC	GACTCCTCTC	AGTCCTTGTC	1560
CACCGCCTTC	CACCCCTCCC	CTCCCCCTTG	CCATAGAGTT	CCAGACATAT	TTTCCGATCA	1620
AGCTTTTATT	TTTTAAAAG	TCAAAACAGA	ACAAAAAAA	AAAAAAA	GAAGAAATAC	1680
GAAGAGACAG	CGTTTGCAGC	CTACCTGGAG	GCCGGGGGGG	AGGGGGCTTA	GGGTGATGGC	1740
CTCCCCCACA	GCGTGGCAA	GGATCTTGGG	ACTAACCAA	TGTCACATCT	GGTCTATAGA	1800
GTCCACCAAA	GAGTCCTCTG	AGTCTTGAGG	GAGATCTTCT	GGATCCTTCT	ACCCTGTCTC	1860
GCTCTCCTAT	CCCACACAG	CTGCCAGCAG	CTGCCCATGT	CACCTGAGCC	TGGCTTCCTA	1920
AACTCTCCTG	TCCCCCTCTCC	TGTCCCCCTT	CAACGCCCC	TTCTCTTAAA	GGGCCCCCAA	1980
TCTTTAGTCT	TCCACTCTGC	CCTGGGGGTG	CTTTCTCTT	CCCAGCCCTG	TCCAGTGAGG	2040
CTGGGGGAGA	AGGCTGCGGA	GGGGAGGGGA	GTGTCTCTC	ACTCCCCAG	ACATGAAGGC	2100
AGGTGAGTGG	GAGGGAGTCA	TGGCCTCCCT	GGCATAACAGG	AGAGGAAGAA	GGAGAACAGA	2160

CCATCTGACC	AGGCTGTGCA	ACACTCCAA	TGCCAAGCCC	ATTTGAGGGA	TGAAAACCT	2220
AGCTGGGCCT	GTGGGCAGAG	GGCTCCTCCT	CAGAGCCAAT	GAGCATTGC	AGAGACCCCTA	2280
CCTGTCTCTT	TAGTCCTTGG	CAATGGGCAA	AGCCTCTTCC	TTGGAAAGTC	CAGGGCAAAG	2340
CCAGCAACAG	TAGCAACCTC	CTCTCACTCT	GGGGAGGAGG	CATTGCCAC	CCATCCCCCT	2400
CCCTTCATGG	TCATTCAGAA	ACGCCACAGC	CCCTCCCATC	CCCAATCACT	GTGTCAGCAT	2460
CAGCCTTTGT	GAAGACGGTC	TACAAGGCTC	TCACCTGGCC	AACCTAGGAG	ATTCAAGGGC	2520
TCAGGAACCT	AGGAGATTCA	GGGGCTTGGG	GAACCTCCAC	CTTGGCACTG	TAAGGGGAAG	2580
CCAGCAGCTC	AGGCTGGTGT	GAGGAAGGAA	CTCTGGATGG	TCACTGTAGC	TTTCTTCCTT	2640
GACCTTTAG	TCCCCAACAT	CCCCTCTGAA	TGCTGGCAGC	ACCCCCACCC	CCACACACAC	2700
ACTCCCATT	CTCTAACGCCC	GAGAGTCTTG	AGTCTTCATT	AAAGGATTCT	GGGTGTGGGA	2760
GGGGACACAG	GGCCTTGTGG	TTGGGAAGCA	GGTGGCAGGC	TCTCCCTTGG	GAGGATGGGG	2820
TGGGAAACGA	AACAGGTCAA	CCAAGACCTC	TTACAGTGGA	AAAGTGGTCAG	AGGCTGTTTC	2880
TTTGGACCTT	TGGGAACACA	GATTGAGAA	AGTCTCATAT	TCACAGCTGG	TGTCCGCTAG	2940
GCTCTGGCC	TACGGACACC	CTCTGCCTTG	TGAATCAGGT	GACCTTTGG	GCCTCCAGGG	3000
AAAGAACAGG	ACCACCATCC	ATGTTCTCCG	CGTCCCTTA	GCTCTCTGCT	GCTTCTCCTG	3060
ACACTCAGGT	CATGGACCCA	AGCTTGGGG	TCCTGACCAC	CGCCCCCCCC	CACCCCCCTT	3120
CTCTTGACTA	GGCTGCAGCA	GGGCCTCTG	TTGGGTCACT	CCTCCTCAGG	GCCAGGAGCA	3180
GGAACCTAGC	ACTCAAGAGA	CAGGGCTGTA	AGCACCCACT	TCCCTGTCAC	TGTTTGCCCT	3240
TGGGGCTTCA	GCTGCAGCCC	AGGTTGGGCC	CTGGAGCCCT	CAGAACCGGA	AGCAGGATTTC	3300
AAACCTCCCC	TTCTCCACAG	CCCCCCCTGC	CTCCCCAGAT	GGTAGACATC	CCCCAGCTCT	3360
TACCTTCACC	CTCATCTCAG	AAAGGCAAGA	AGCCGCCATG	TCCGCACCTT	GGGGCTGGG	3420
CTTCCCCCTC	TCTGTGCCAG	CGGTTCCCAG	CACCTGGGG	GGGGCTGTGG	CCTGACCAGA	3480
CCCCAGGCC	ACCCCACATA	GTATACTAGC	TGCCCACCT	GGGGCAGGAA	CTGGAAAATC	3540
CATCCCTTTT	GAACAACCAC	CTTCAATGAC	CCCCCCCAC	TGGGACCAGA	CTTGGTCCTC	3600
AAGTTATTCA	GCACCCCCAG	TGCAGGAGGG	TCCTCCCCC	ACCCCCCGAA	GTCCCTGGAG	3660
CCCGGAGCAG	AGCCCCACCT	GTGATTCTTG	GTGTTAGGGC	ACCTCAAACC	TTGGGCTGGA	3720
CCACACCCCT	TCCCGCCATT	TCCAGACCCC	TACCTGTACT	CCCCAGTGCT	CCCCAGGGC	3780
CTCTTGATGC	TGCACGGGAC	CCTGCAGGGC	TCGGTCAGTG	ATGTGTTTG	TCCCCAGTTA	3840
ACCGCCATCC	AGCGACCTGG	TTCCAGGAGG	AGCTCAGGTC	ACCCCCACCA	CCGCCGCCAC	3900
TGCGTCTGCC	GCCCTAGGCT	TTCAGACATC	ATTAGTCCG	ACACTGTGA	AACTCCGAGA	3960
CGTGCCGTGG	TCTCAGCAAT	GCACCTGTT	TATACATGAT	TGTGTAATTT	AAAGGTATAT	4020
AAATACAAAT	ATATATATTA	TATCTATATC	TATCAGTTGT	GACCGTATGG	CTGTCGATAA	4080
AACCAGAATT	C					4091

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ser Gly Ser Tyr Asp Glu Ala Ser Glu Glu Ile Thr Asp Ser Phe
1 5 10 15

Trp Glu Val Gly Asn Tyr Lys Arg Thr Val Lys Arg Ile Asp Asp Gly
20 25 30

His Arg Leu Cys Asn Asp Leu Met Ser Cys Val Gln Glu Arg Ala Lys
35 40 45

Ile Glu Lys Ala Tyr Ala Gln Gln Leu Thr Asp Trp Ala Lys Arg Trp
50 55 60

Arg Gln Leu Ile Glu Lys Gly Pro Gln Tyr Gly Ser Leu Glu Arg Ala
65 70 75 80

Trp Gly Ala Met Met Thr Glu Ala Asp Lys Val Ser Glu Leu His Gln
85 90 95

Glu Val Lys Asn Ser Leu Leu Asn Glu Asp Leu Glu Lys Val Lys Asn
100 105 110

Trp Gln Lys Asp Ala Tyr His Lys Gln Ile Met Gly Gly Phe Lys Glu
115 120 125

Thr Lys Glu Ala Glu Asp Gly Phe Arg Lys Ala Gln Lys Pro Trp Ala
130 135 140

Lys Lys Met Lys Glu Leu Glu Ala Ala Lys Lys Ala Tyr His Leu Ala
145 150 155 160

Cys Lys Glu Glu Arg Leu Ala Met Thr Arg Glu Met Asn Ser Lys Thr
165 170 175

Glu Gln Ser Val Thr Pro Glu Gln Gln Lys Lys Leu Val Asp Lys Val
180 185 190

Asp Lys Cys Arg Gln Asp Val Gln Lys Thr Gln Glu Lys Tyr Glu Lys
195 200 205

Val Leu Glu Asp Val Gly Lys Thr Thr Pro Gln Tyr Met Glu Gly Met
210 215 220

Glu Gln Val Phe Glu Gln Cys Gln Gln Phe Glu Glu Lys Arg Leu Val
225 230 235 240

Phe Leu Lys Glu Val Leu Leu Asp Ile Lys Arg His Leu Asn Leu Ala
245 250 255

Glu Asn Ser Ser Tyr Met His Val Tyr Arg Glu Leu Glu Gln Ala Ile
260 265 270

Arg Gly Ala Asp Ala Gln Glu Asp Leu Arg Trp Phe Arg Ser Thr Ser
275 280 285

Gly Pro Gly Met Pro Met Asn Trp Pro Gln Phe Glu Glu Trp Asn Pro

290

295

300

Asp	Leu	Pro	His	Thr	Thr	Ala	Lys	Lys	Glu	Lys	Gln	Pro	Lys	Lys	Ala
305						310			315			320			
Glu	Gly	Ala	Thr	Leu	Ser	Asn	Ala	Thr	Gly	Ala	Val	Glu	Ser	Thr	Ser
				325					330			335			
Gln	Ala	Gly	Asp	Arg	Gly	Ser	Val	Ser	Ser	Tyr	Asp	Arg	Gly	Gln	Thr
				340				345			350				
Tyr	Ala	Thr	Glu	Trp	Ser	Asp	Asp	Glu	Ser	Gly	Asn	Pro	Phe	Gly	Gly
				355				360			365				
Asn	Glu	Ala	Asn	Gly	Gly	Ala	Asn	Pro	Phe	Glu	Asp	Asp	Ala	Lys	Gly
				370			375			380					
Val	Arg	Val	Arg	Ala	Leu	Tyr	Asp	Tyr	Asp	Gly	Gln	Glu	Gln	Asp	Glu
				385		390			395			400			
Leu	Ser	Phe	Lys	Ala	Gly	Asp	Glu	Leu	Thr	Lys	Leu	Gly	Glu	Glu	Asp
				405					410			415			
Glu	Gln	Gly	Trp	Cys	Arg	Gly	Arg	Leu	Asp	Ser	Gly	Gln	Leu	Gly	Leu
				420				425			430				
Tyr	Pro	Ala	Asn	Tyr	Val	Glu	Ala	Ile							
				435			440								

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1133 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GAATTCTCG	ACCCACGGTC	CGGGAAAGCCT	TTCACAAGCA	GATGATGGC	GGCTTCAAGG	60
AGACCAAGGA	AGCTGAGGAC	GGCTTTCGGA	AGGCACAGAA	GCCCTGGCC	AAGAAGCTGA	120
AAGAGGTAGA	AGCAGCAAAG	AAAGCCCACC	ATGCAGCGTG	CAAAGAGGAG	AAGCTGGCTA	180
TCTCACGAGA	AGCCAACAGC	AAGGCAGACC	CATCCCCTCAA	CCCTGAACAG	CTCAAGAAAT	240
TGCAAGACAA	AATAGAAAAG	TGCAAGCAAG	ATGTTCTTAA	GACCAAAGAG	AAGTATGAGA	300
AGTCCCTGAA	GGAACTCGAC	CAGGGCACAC	CCCAGTACAT	GGAGAACATG	GAGCAGGTGT	360
TTGAGCAGTG	CCAGCAGTTC	GAGGAGAAC	GCCTTCGCTT	CTTCCGGAG	GTTCTGCTGG	420
AGGTTCAGAA	GCACCTAGAC	CTGTCCAATG	TGGCTGGTTA	CAAAGCCATT	TACCATGACC	480
TGGAGCAGAG	CATCAGAGCA	GCTGATGCAG	TGGAGGACCT	GAGGTGGTTC	CGAGCCAATC	540
ACGGGCCGGG	CATGGCCATG	AACTGGCCGC	AGTTGAGGA	GTGGTCCGCA	GACCTGAATC	600
GAACCCCTCAG	CCGGAGAGAG	AAGAAGAAGT	CCACTGACGG	CGTCACCCCTG	ACGGGCATCA	660
ACCAGACAGG	CGACCAGTCT	CTGCCGAGTA	AGCCCAGCAG	CACCCCTTAAT	GTCCCGAGCA	720
ACCCCGCCCA	GTCTGCGCAG	TCACAGTCCA	GCTACAACCC	CTTCGAGGAT	GAGGACGACA	780

CGGGCAGCAC CGTCAGTGAG AAGGACGACA CTAAGGCCAA AAATGTGAGC AGCTACGAGA	840
AGACCCAGAG CTATCCCACC GACTGGTCAG ACGATGAGTC TAACAACCCC TTCTCCTCCA	900
CGGATGCCAA TGGGGACTCG AATCCATTG ACGACGACGC CACCTCGGGG ACGGAAGTGC	960
GAGTCCGGGC CCTGTATGAC TATGAGGGC AGGAGCATGA TGAGCTGAGC TTCAAGGCTG	1020
GGGATGAGCT GACCAAGATG GAGGACGAGG ATGAGCAGGG CTGGTGCAAG GGACGCTTGG	1080
ACAAACGGGCA AGTTGGCCTA TACCCGGCAA ATTATGTGGA GGCGATCCAG TGA	1133

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Arg Ile Arg Arg Pro Thr Val Arg Glu Ala Phe His Lys Gln Met Met
 1 5 10 15

Gly Gly Phe Lys Glu Thr Lys Glu Ala Glu Asp Gly Phe Arg Lys Ala
 20 25 30

Gln Lys Pro Trp Ala Lys Lys Leu Lys Glu Val Glu Ala Ala Lys Lys
 35 40 45

Ala His His Ala Ala Cys Lys Glu Glu Lys Leu Ala Ile Ser Arg Glu
 50 55 60

Ala Asn Ser Lys Ala Asp Pro Ser Leu Asn Pro Glu Gln Leu Lys Lys
 65 70 75 80

Leu Gln Asp Lys Ile Glu Lys Cys Lys Gln Asp Val Leu Lys Thr Lys
 85 90 95

Glu Lys Tyr Glu Lys Ser Leu Lys Glu Leu Asp Gln Gly Thr Pro Gln
 100 105 110

Tyr Met Glu Asn Met Glu Gln Val Phe Glu Gln Cys Gln Gln Phe Glu
 115 120 125

Glu Lys Arg Leu Arg Phe Phe Arg Glu Val Leu Glu Val Gln Lys
 130 135 140

His Leu Asp Leu Ser Asn Val Ala Gly Tyr Lys Ala Ile Tyr His Asp
 145 150 155 160

Leu Glu Gln Ser Ile Arg Ala Ala Asp Ala Val Glu Asp Leu Arg Trp
 165 170 175

Phe Arg Ala Asn His Gly Pro Gly Met Ala Met Asn Trp Pro Gln Phe
 180 185 190

Glu Glu Trp Ser Ala Asp Leu Asn Arg Thr Leu Ser Arg Arg Glu Lys
 195 200 205

Lys Lys Ser Thr Asp Gly Val Thr Leu Thr Gly Ile Asn Gln Thr Gly
 210 215 220

Asp	Gln	Ser	Leu	Pro	Ser	Lys	Pro	Ser	Ser	Thr	Leu	Asn	Val	Pro	Ser
225					230					235				240	
Asn	Pro	Ala	Gln	Ser	Ala	Gln	Ser	Gln	Ser	Ser	Tyr	Asn	Pro	Phe	Glu
	245					250					255				
Asp	Glu	Asp	Asp	Thr	Gly	Ser	Thr	Val	Ser	Glu	Lys	Asp	Asp	Thr	Lys
	260					265					270				
Ala	Lys	Asn	Val	Ser	Ser	Tyr	Glu	Lys	Thr	Gln	Ser	Tyr	Pro	Thr	Asp
	275				280					285					
Trp	Ser	Asp	Asp	Glu	Ser	Asn	Asn	Pro	Phe	Ser	Ser	Thr	Asp	Ala	Asn
	290				295				300						
Gly	Asp	Ser	Asn	Pro	Phe	Asp	Asp	Asp	Ala	Thr	Ser	Gly	Thr	Glu	Val
	305				310				315			320			
Arg	Val	Arg	Ala	Leu	Tyr	Asp	Tyr	Glu	Gly	Gln	Glu	His	Asp	Glu	Leu
	325					330					335				
Ser	Phe	Lys	Ala	Gly	Asp	Glu	Leu	Thr	Lys	Met	Glu	Asp	Glu	Asp	Glu
	340					345					350				
Gln	Gly	Trp	Cys	Lys	Gly	Arg	Leu	Asp	Asn	Gly	Gln	Val	Gly	Leu	Tyr
	355					360					365				
Pro	Ala	Asn	Tyr	Val	Glu	Ala	Ile	Gln							
	370				375										

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1400 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Ala	Ala	Ala	Ala	Gly	Gly	Ala	Gly	Ala	Gly	Ala	Thr	Gly			
1				5			10				15				
Thr	Cys	Ala	Ala	Ala	Ala	Gly	Ala	Ala	Gly	Gly	Ala	Thr	Gly	Gly	
	20				25						30				
Cys	Gly	Ala	Gly	Gly	Ala	Ala	Ala	Ala	Gly	Gly	Cys	Ala	Ala	Ala	
	35				40				45						
Cys	Ala	Gly	Gly	Ala	Ala	Gly	Cys	Ala	Cys	Ala	Gly	Ala	Cys	Ala	
	50				55			60							
Ala	Gly	Cys	Thr	Gly	Gly	Thr	Cys	Gly	Gly	Cys	Thr	Thr	Thr	Thr	
	65			70			75			80					
Cys	Cys	Ala	Thr	Cys	Ala	Ala	Cys	Ala	Cys	Ala	Gly	Ala	Ala		
	85			90					95						
Cys	Cys	Ala	Gly	Cys	Thr	Ala	Ala	Gly	Cys	Cys	Ala	Gly	Cys	Thr	Gly
	100			105				110							
Thr	Cys	Cys	Ala	Gly	Gly	Cys	Ala	Cys	Cys	Cys	Thr	Gly	Gly	Thr	Cys
	115			120						125					

Cys Ala Cys Thr Gly Cys Ala Gly Ala Ala Ala Ala Ala Gly Gly Gly
130 135 140

Thr Cys Cys Ala Cys Thr Thr Ala Cys Cys Ala Thr Thr Thr Cys Thr
145 150 155 160

Gly Cys Ala Cys Ala Gly Gly Ala Ala Ala Ala Thr Gly Thr Ala Ala
165 170 175

Ala Ala Gly Thr Gly Gly Thr Gly Thr Ala Thr Thr Ala Cys Cys Gly
180 185 190

Gly Gly Cys Ala Cys Thr Gly Thr Ala Cys Cys Cys Thr Thr Thr
195 200 205

Gly Ala Ala Thr Cys Cys Ala Gly Ala Ala Gly Cys Cys Ala Thr Gly
210 215 220

Ala Thr Gly Ala Ala Ala Thr Cys Ala Cys Thr Ala Thr Cys Cys Ala
225 230 235 240

Gly Cys Cys Ala Gly Gly Ala Gly Ala Cys Ala Thr Ala Gly Thr Cys
245 250 255

Ala Thr Gly Gly Thr Gly Ala Thr Gly Ala Ala Ala Gly Cys Cys
260 265 270

Ala Ala Ala Cys Thr Gly Gly Ala Gly Ala Ala Cys Cys Cys Gly Gly
275 280 285

Cys Thr Gly Gly Cys Thr Thr Gly Gly Ala Gly Gly Ala Gly Ala Ala
290 295 300

Thr Thr Ala Ala Ala Ala Gly Gly Ala Ala Ala Gly Ala Cys Ala Gly
305 310 315 320

Gly Gly Thr Gly Gly Thr Thr Cys Cys Cys Thr Gly Cys Ala Ala Ala
325 330 335

Cys Thr Ala Thr Gly Cys Ala Gly Ala Gly Ala Ala Ala Ala Thr Cys
340 345 350

Cys Cys Ala Gly Ala Ala Ala Ala Thr Gly Ala Gly Gly Thr Thr Cys
355 360 365

Cys Cys Gly Cys Thr Cys Cys Ala Gly Thr Gly Ala Ala Ala Cys Cys
370 375 380

Ala Gly Thr Gly Ala Cys Thr Gly Ala Thr Thr Cys Ala Ala Cys Ala
385 390 395 400

Thr Cys Thr Gly Cys Cys Cys Cys Thr Gly Cys Cys Cys Cys Cys Ala
405 410 415

Ala Ala Cys Thr Gly Gly Cys Cys Thr Thr Gly Cys Gly Thr Gly Ala
420 425 430

Gly Ala Cys Cys Cys Cys Cys Gly Cys Cys Cys Cys Thr Thr Thr Gly
435 440 445

Gly Cys Ala Gly Thr Ala Ala Cys Cys Thr Cys Thr Thr Cys Ala Gly
450 455 460

Ala Gly Cys Cys Cys Thr Cys Cys Ala Cys Gly Ala Cys Cys Cys Cys
465 470 475 480

Thr Ala Ala Thr Ala Ala Cys Thr Gly Gly Cys Cys Gly Ala Cys

485

490

495

Thr Thr Cys Ala Gly Cys Thr Cys Cys Ala Cys Gly Thr Gly Gly Cys
 500 505 510

Cys Cys Ala Cys Cys Ala Gly Cys Ala Cys Gly Ala Ala Thr Gly Ala
 515 520 525

Gly Ala Ala Ala Cys Cys Ala Gly Ala Ala Ala Cys Gly Gly Ala Thr
 530 535 540

Ala Ala Cys Thr Gly Gly Ala Thr Gly Cys Ala Thr Gly Gly Gly
 545 550 555 560

Cys Ala Gly Cys Cys Cys Ala Gly Cys Cys Cys Thr Cys Thr Cys Thr
 565 570 575

Cys Ala Cys Cys Gly Thr Thr Cys Cys Ala Ala Gly Thr Gly Cys Cys
 580 585 590

Gly Gly Cys Cys Ala Gly Thr Thr Ala Ala Gly Gly Cys Ala Gly Ala
 595 600 605

Gly Gly Thr Cys Cys Gly Cys Cys Thr Thr Ala Cys Thr Cys Cys
 610 615 620

Ala Gly Cys Cys Ala Cys Gly Gly Cys Cys Ala Cys Thr Gly Gly Cys
 625 630 635 640

Thr Cys Cys Thr Cys Cys Cys Gly Thr Cys Thr Cys Cys Thr Gly
 645 650 655

Thr Gly Cys Thr Ala Gly Gly Cys Cys Ala Gly Gly Gly Thr Gly Ala
 660 665 670

Ala Ala Ala Gly Gly Thr Gly Gly Ala Gly Gly Gly Cys Thr Ala
 675 680 685

Cys Ala Ala Gly Cys Thr Cys Ala Ala Gly Cys Cys Cys Thr Ala Thr
 690 695 700

Ala Thr Cys Cys Thr Thr Gly Gly Ala Gly Ala Gly Cys Cys Ala Ala
 705 710 715 720

Ala Ala Ala Ala Gly Ala Cys Ala Ala Cys Cys Ala Cys Thr Thr Ala
 725 730 735

Ala Ala Thr Thr Thr Ala Ala Cys Ala Ala Ala Ala Ala Thr Gly
 740 745 750

Ala Thr Gly Thr Cys Ala Thr Cys Ala Cys Cys Gly Thr Cys Cys Thr
 755 760 765

Gly Gly Ala Ala Cys Ala Gly Cys Ala Ala Gly Ala Cys Ala Thr Gly
 770 775 780

Thr Gly Gly Thr Gly Gly Thr Thr Gly Gly Ala Gly Ala Ala Gly
 785 790 795 800

Thr Thr Cys Ala Ala Gly Gly Thr Cys Ala Gly Ala Ala Gly Gly
 805 810 815

Thr Thr Gly Gly Thr Thr Cys Cys Cys Ala Ala Gly Thr Cys Thr
 820 825 830

Thr Ala Cys Gly Thr Gly Ala Ala Ala Cys Thr Cys Ala Thr Thr Thr
 835 840 845

Cys Ala Gly Gly Gly Cys Cys Ala Thr Ala Ala Gly Gly Ala Ala
 850 855 860
 Gly Thr Cys Thr Ala Cys Ala Ala Gly Cys Ala Thr Gly Gly Ala Thr
 865 870 875 880
 Thr Cys Thr Gly Gly Thr Thr Cys Thr Thr Cys Ala Gly Ala Gly Ala
 885 890 895
 Gly Thr Cys Cys Thr Gly Cys Thr Ala Gly Thr Cys Thr Ala Ala Ala
 900 905 910
 Gly Cys Gly Ala Gly Thr Ala Gly Cys Cys Thr Cys Thr Cys Cys Ala
 915 920 925
 Gly Cys Ala Gly Cys Cys Ala Ala Gly Cys Cys Gly Ala Gly Cys Cys
 930 935 940
 Ala Ala Gly Cys Cys Gly Gly Thr Cys Gly Thr Thr Thr Cys Gly Gly
 945 950 955 960
 Gly Ala Gly Ala Ala Gly Ala Ala Ala Thr Thr Gly Cys Cys Cys Ala
 965 970 975
 Gly Gly Thr Thr Ala Thr Thr Gly Cys Cys Thr Cys Ala Thr Ala Cys
 980 985 990
 Ala Cys Cys Gly Cys Cys Ala Cys Cys Gly Gly Cys Cys Cys Gly
 995 1000 1005
 Ala Gly Cys Ala Gly Cys Thr Cys Ala Cys Thr Cys Thr Cys Gly Cys
 1010 1015 1020
 Cys Cys Cys Thr Gly Gly Thr Cys Ala Gly Cys Thr Gly Ala Thr Thr
 1025 1030 1035 1040
 Thr Thr Gly Ala Thr Cys Cys Gly Ala Ala Ala Ala Ala Gly Ala
 1045 1050 1055
 Ala Cys Cys Cys Ala Gly Gly Thr Gly Gly Ala Thr Gly Gly Thr Gly
 1060 1065 1070
 Gly Gly Ala Ala Gly Gly Ala Gly Ala Gly Cys Thr Gly Cys Ala Ala
 1075 1080 1085
 Gly Cys Ala Cys Gly Thr Gly Gly Ala Ala Ala Ala Ala Gly Cys
 1090 1095 1100
 Gly Cys Cys Ala Gly Ala Thr Ala Gly Gly Cys Thr Gly Gly Thr Thr
 1105 1110 1115 1120
 Cys Cys Cys Ala Gly Cys Thr Ala Ala Thr Thr Ala Thr Gly Thr Ala
 1125 1130 1135
 Ala Ala Gly Cys Thr Thr Cys Thr Ala Ala Gly Cys Cys Thr Gly
 1140 1145 1150
 Gly Gly Ala Cys Gly Ala Gly Cys Ala Ala Ala Ala Thr Cys Ala Cys
 1155 1160 1165
 Thr Cys Cys Ala Ala Cys Ala Gly Ala Gly Cys Cys Ala Cys Cys Thr
 1170 1175 1180
 Ala Ala Gly Thr Cys Ala Ala Cys Ala Gly Cys Ala Thr Thr Ala Gly
 1185 1190 1195 1200
 Cys Gly Gly Cys Ala Gly Thr Gly Thr Cys Cys Cys Ala Gly Gly Thr

1205	1210	1215
Gly Ala Thr Thr Gly Gly Gly Ala Thr Gly Thr Ala Cys Gly Ala Cys		
1220	1225	1230
Thr Ala Cys Ala Cys Cys Gly Cys Gly Cys Ala Gly Ala Ala Thr Gly		
1235	1240	1245
Ala Cys Gly Ala Thr Gly Ala Gly Cys Thr Gly Gly Cys Cys Thr Thr		
1250	1255	1260
Cys Ala Ala Cys Ala Ala Gly Gly Gly Cys Cys Ala Gly Ala Thr Cys		
1265	1270	1275
Ala Thr Cys Ala Ala Cys Gly Thr Cys Cys Thr Cys Ala Ala Cys Ala		
1285	1290	1295
Ala Gly Gly Ala Gly Gly Ala Cys Cys Cys Thr Gly Ala Cys Thr Gly		
1300	1305	1310
Gly Thr Gly Gly Ala Ala Ala Gly Gly Ala Gly Ala Ala Gly Thr Cys		
1315	1320	1325
Ala Ala Thr Gly Gly Ala Cys Ala Ala Gly Thr Gly Gly Gly Cys		
1330	1335	1340
Thr Cys Thr Thr Cys Cys Cys Ala Thr Cys Cys Ala Ala Thr Thr Ala		
1345	1350	1355
1360		
Thr Gly Thr Gly Ala Ala Gly Cys Thr Gly Ala Cys Cys Ala Cys Ala		
1365	1370	1375
Gly Ala Cys Ala Thr Gly Gly Ala Cys Cys Cys Ala Ala Gly Cys Cys		
1380	1385	1390
Ala Gly Cys Ala Ala Thr Gly Ala		
1395	1400	

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Lys	Gly	Arg	Arg	Val	Ser	Lys	Arg	Arg	Met	Ala	Arg	Lys	Lys	Ala	Asn
1				5					10					15	
Arg	Lys	His	Lys	Thr	Ser	Trp	Val	Gly	Phe	Ser	Ile	Asn	Thr	Lys	Asn
				20			25					30			
Gln	Leu	Ser	Gln	Leu	Ser	Arg	His	Pro	Gly	Pro	Leu	Gln	Lys	Lys	Gly
				35		40					45				
Pro	Leu	Thr	Ile	Ser	Ala	Gln	Glu	Asn	Val	Lys	Val	Val	Tyr	Tyr	Arg
				50		55			60						
Ala	Leu	Tyr	Pro	Phe	Glu	Ser	Arg	Ser	His	Asp	Glu	Ile	Thr	Ile	Gln
				65		70			75			80			
Pro	Gly	Asp	Ile	Val	Met	Val	Asp	Glu	Ser	Gln	Thr	Gly	Glu	Pro	Gly

85

90

95

Trp Leu Gly Gly Glu Leu Lys Gly Lys Thr Gly Trp Phe Pro Ala Asn
 100 105 110

Tyr Ala Glu Lys Ile Pro Glu Asn Glu Val Pro Ala Pro Val Lys Pro
 115 120 125

Val Thr Asp Ser Thr Ser Ala Pro Ala Pro Lys Leu Ala Leu Arg Glu
 130 135 140

Thr Pro Ala Pro Leu Ala Val Thr Ser Ser Glu Pro Ser Thr Thr Pro
 145 150 155 160

Asn Asn Trp Ala Asp Phe Ser Ser Thr Trp Pro Thr Ser Thr Asn Glu
 165 170 175

Lys Pro Glu Thr Asp Asn Trp Asp Ala Trp Ala Ala Gln Pro Ser Leu
 180 185 190

Thr Val Pro Ser Ala Gly Gln Leu Arg Gln Arg Ser Ala Phe Thr Pro
 195 200 205

Ala Thr Ala Thr Gly Ser Ser Pro Ser Pro Val Leu Gly Gln Gly Glu
 210 215 220

Lys Val Glu Gly Leu Gln Ala Gln Ala Leu Tyr Pro Trp Arg Ala Lys
 225 230 235 240

Lys Asp Asn His Leu Asn Phe Asn Lys Asn Asp Val Ile Thr Val Leu
 245 250 255

Glu Gln Gln Asp Met Trp Trp Phe Gly Glu Val Gln Gly Gln Lys Gly
 260 265 270

Trp Phe Pro Lys Ser Tyr Val Lys Leu Ile Ser Gly Pro Ile Arg Lys
 275 280 285

Ser Thr Ser Met Asp Ser Gly Ser Ser Glu Ser Pro Ala Ser Leu Lys
 290 295 300

Arg Val Ala Ser Pro Ala Ala Lys Pro Val Val Ser Gly Glu Glu Ile
 305 310 315 320

Ala Gln Val Ile Ala Ser Tyr Thr Ala Thr Gly Pro Glu Gln Leu Thr
 325 330 335

Leu Ala Pro Gly Gln Leu Ile Leu Ile Arg Lys Lys Asn Pro Gly Gly
 340 345 350

Trp Trp Glu Gly Glu Leu Gln Ala Arg Gly Lys Lys Arg Gln Ile Gly
 355 360 365

Trp Phe Pro Ala Asn Tyr Val Lys Leu Leu Ser Pro Gly Thr Ser Lys
 370 375 380

Ile Thr Pro Thr Glu Pro Pro Lys Ser Thr Ala Leu Ala Ala Val Cys
 385 390 395 400

Gln Val Ile Gly Met Tyr Asp Tyr Thr Ala Gln Asn Asp Asp Glu Leu
 405 410 415

Ala Phe Asn Lys Gly Gln Ile Ile Asn Val Leu Asn Lys Glu Asp Pro
 420 425 430

Asp Trp Trp Lys Gly Glu Val Asn Gly Gln Val Gly Leu Phe Pro Ser
 435 440 445

Asn Tyr Val Lys Leu Thr Thr Asp Met Asp Pro Ser Gln Gln
 450 455 460

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GAATTCGCGG CCGCGTCGAC CAAGATCATT CCTGGGAGTG AAGTAAAACG GGAAGAACCA	60
GAAGCTTGT ATGCAGCTGT AAATAAGAAA CCTACCTCGG CAGCCTATTC AGTTGGAGAA	120
GAATATATTG CACTTTATCC ATATTCAAGT GTGGAACCTG GAGATTGAC TTTCACAGAA	180
GGTGAAGAAA TATTGGTGAC CCAGAAAGAT GGAGAGTGGT GGACAGGAAG TATTGGAGAT	240
AGAAAGTGGAA TTTTCCATC AAACATATGTC AAACCAAAGG ATCAAGAGAG TTTTGGGAGT	300
GCTAGCAAGT CTGGAGCATC AAATAAAAAAA CCTGAGATTG CTCAGGTAAC TTCAGCATAT	360
GTTGCTTCTG GTTCTGAACA ACTTAGCCTT GCACCAGGAC AGTTAATATT AATTCTAAAG	420
AAAAATACAA GTGGGTGGTG GCAAGGAGAG TTACAGGCCA GAGGAAAAAA GCGACAGAAA	480
GGATGGTTTC CTGCCAGTCA TGTTAAACTT TTGGGTCCAA GCAGTGAAAG AGCCACACCT	540
GCCTTCATC CTGTATGTCA GGTGATTGCT ATGTATGACT ATGCAGCAAA TAATGAAGAT	600
GAGCTCAGTT TCTCCAAGGG ACAACTCATT AATGTTATGA ACAAAAGATGA TCCTGATTGG	660
TGGCAAGGAG AGATCAACGG GGTGACTGGT CTCTTCCCTT CAAACTACGT TAAGATGACC	720
ACAGACTCAG ATCCAAGTCA ACAGTGA	747

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Glu Phe Ala Ala Ala Ser Thr Lys Ile Ile Pro Gly Ser Glu Val Lys	
1 5 10 15	
Arg Glu Glu Pro Glu Ala Leu Tyr Ala Ala Val Asn Lys Lys Pro Thr	
20 25 30	
Ser Ala Ala Tyr Ser Val Gly Glu Glu Tyr Ile Ala Leu Tyr Pro Tyr	
35 40 45	
Ser Ser Val Glu Pro Gly Asp Leu Thr Phe Thr Glu Gly Glu Glu Ile	
50 55 60	

Leu Val Thr Gln Lys Asp Gly Glu Trp Trp Thr Gly Ser Ile Gly Asp
 65 70 75 80

Arg Ser Gly Ile Phe Pro Ser Asn Tyr Val Lys Pro Lys Asp Gln Glu
 85 90 95

Ser Phe Gly Ser Ala Ser Lys Ser Gly Ala Ser Asn Lys Lys Pro Glu
 100 105 110

Ile Ala Gln Val Thr Ser Ala Tyr Val Ala Ser Gly Ser Glu Gln Leu
 115 120 125

Ser Leu Ala Pro Gly Gln Leu Ile Leu Ile Leu Lys Lys Asn Thr Ser
 130 135 140

Gly Trp Trp Gln Gly Glu Leu Gln Ala Arg Gly Lys Lys Arg Gln Lys
 145 150 155 160

Gly Trp Phe Pro Ala Ser His Val Lys Leu Leu Gly Pro Ser Ser Glu
 165 170 175

Arg Ala Thr Pro Ala Phe His Pro Val Cys Gln Val Ile Ala Met Tyr
 180 185 190

Asp Tyr Ala Ala Asn Asn Glu Asp Glu Leu Ser Phe Ser Lys Gly Gln
 195 200 205

Leu Ile Asn Val Met Asn Lys Asp Asp Pro Asp Trp Trp Gln Gly Glu
 210 215 220

Ile Asn Gly Val Thr Gly Leu Phe Pro Ser Asn Tyr Val Lys Met Thr
 225 230 235 240

Thr Asp Ser Asp Pro Ser Gln Gln
 245

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Other
 - (D) OTHER INFORMATION: Biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ser Gly Ser Gly Ser Arg Pro Pro Arg Trp Ser Pro Pro Pro Val Pro
 1 5 10 15

Leu Pro Thr Ser Leu Asp Ser Arg
 20

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: Other
(D) OTHER INFORMATION: Biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Ser Gly Ser Gly Val Leu Lys Arg Pro Leu Pro Ile Pro Pro Val Thr
1 5 10 15
Arg

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: Other
(D) OTHER INFORMATION: Biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ser Glu Ser Gly Ser Arg Leu Gly Glu Phe Ser Lys Pro Pro Ile Pro
1 5 10 15
Gln Lys Pro Thr Trp Met Ser Arg
20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: Other
(D) OTHER INFORMATION: Biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Ser Thr Val Pro Arg Trp Ile Glu Asp Ser Leu Arg Gly Gly Ala Ala
1 5 10 15
Arg Ala Gln Thr Arg Leu Ala Ser Ala Lys
20 25

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Arg Pro Leu Pro Pro Leu Pro
1 5

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Cys Trp Ser Glu Trp Asp Gly Asn Glu Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Cys Gly Gln Trp Ala Asp Asp Gly Tyr Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 3
- (D) OTHER INFORMATION: Undefined

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Cys Glu Xaa Trp Asp Gly Tyr Gly Ala Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Cys Trp Pro Phe Trp Asp Gly Ser Thr Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Cys Met Ile Trp Pro Asp Gly Glu Glu Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 4
- (D) OTHER INFORMATION: Undefined

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Cys Glu Ser Xaa Trp Asp Gly Tyr Asp Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Cys Gln Gln Trp Lys Glu Asp Gly Trp Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 4
 (D) OTHER INFORMATION: Undefined

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Cys Leu Tyr Xaa Trp Asp Gly Tyr Glu Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Cys Met Gly Asp Asn Leu Gly Asp Asp Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

 (A) NAME/KEY: Other
 (B) LOCATION: 8
 (D) OTHER INFORMATION: Undefined

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Cys Met Gly Asp Ser Leu Gly Xaa Ser Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Cys Met Asp Asp Asp Leu Gly Lys Gly Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Cys Met Gly Glu Asn Leu Gly Trp Ser Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Cys Leu Gly Glu Ser Leu Gly Trp Met Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Gly Asp Gly Tyr Glu Glu Ile Ser Pro
1 5

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Gly Asp Gly Tyr Asp Glu Pro Ser Pro
1 5

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Gly Asp Gly Tyr Asp His Pro Ser Pro
1 5

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Gly Asp Gly Tyr Val Ile Pro Ser Pro
1 5

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Gly Asp Gly Tyr Gln Asn Tyr Ser Pro
1 5

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Gly Asp Gly Tyr Met Ala Met Ser Pro
1 5

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Gly Asp Gly Gln Asn Tyr Ser Pro
1 5

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: Other
(D) OTHER INFORMATION: Biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Ser Gly Ser Gly Ser Met Pro Pro Pro Val Pro Pro Arg Pro Pro Gly
1 5 10 15

Thr Leu Gly Gly
20

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: Other
(D) OTHER INFORMATION: Biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Ser Gly Ser Gly Asn Tyr Val Asn Ala Leu Pro Pro Gly Pro Pro Leu
1 5 10 15

Pro Ala Lys Asn Gly Gly
20

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Thr Val Ile Gln Asp Tyr Glu Pro Arg Leu Thr Asp Glu Ile Arg Ile

1	5	10	15												
Ser	Leu	Gly	Glu	Lys	Val	Lys	Ile	Leu	Ala	Thr	His	Thr	Asp	Cys	Leu
			20				25						30		
Val	Glu	Lys	Cys	Asn	Thr	Arg	Lys								
			35				40								

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Arg	Ala	Leu	Phe	Asp	Tyr	Asp	Lys	Thr	Lys	Asp	Cys	Gly	Phe	Leu	Ser
1			5				10						15		
Gln	Ala	Leu	Ser	Phe	Arg	Phe	Gly	Asp	Val	Leu	His	Val	Ile	Asp	Ala
			20				25						30		
Gly	Asp	Glu	Glu	Gln	Ala	Arg	Arg	Val	His	Ser	Asp	Ser	Glu		
			35				40						45		

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Arg	Ala	Gln	Phe	Asp	Tyr	Asp	Pro	Lys	Lys	Asp	Asn	Leu	Ile	Pro	Cys
1			5				10						15		
Lys	Glu	Ala	Gly	Leu	Lys	Phe	Ala	Thr	Gly	Asp	Ile	Ile	Gln	Ile	Ile
			20				25						30		
Asn	Lys	Asp	Asp	Ser	Asn	Gln	Gly	Arg	Val	Glu	Gly	Ser	Ser		
			35				40						45		

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Arg	Thr	His	Pro	His	Tyr	Glu	Lys	Glu	Ser	Pro	Tyr	Gly	Leu	Ser	Phe
1			5				10						15		

Asn Lys Gly Glu Val Phe Arg Ala Val Asp Thr Leu Tyr Asn Gly Lys
20 25 30
Leu Gly Ser Ala Ile Arg Ile Gly Lys Asn His Lys Glu
35 40 45

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Val Ala Ile Lys Ala Tyr Thr Ala Val Glu Gly Asp Glu Val Ser Leu
1 5 10 15
Leu Glu Gly Glu Ala Val Glu Val Ile His Lys Leu Leu Asp Gly Val
20 25 30
Ile Arg Lys Asp Asp Val Thr Gly Tyr
35 40

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Arg Ala Ile Leu Pro Tyr Thr Lys Val Pro Asp Thr Asp Glu Ile Ser
1 5 10 15
Phe Leu Lys Gly Asp Met Phe Ile Val His Asn Glu Leu Glu Asp Met
20 25 30
Trp Val Thr Asn Leu Arg Thr
35

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Arg Ala Val Tyr Ala Tyr Glu Pro Gln Thr Pro Glu Glu Leu Ala Ile
1 5 10 15
Gln Glu Asp Asp Leu Leu Tyr Leu Leu Gln Lys Ser Asp Ile Asp Asp

20

25

30

Thr Val Lys Lys Arg Val Ile Gly Ser Asp
 35 40

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Lys Ala Lys Tyr Ser Tyr Gln Ala Gln Thr Ser Lys Glu Leu Ser Phe
 1 5 10 15
 Met Glu Gly Glu Phe Phe Tyr Val Ser Gly Asp Glu Lys Asp Lys Ala
 20 25 30
 Ser Asn Pro Ser Thr Gly Lys Glu
 35 40

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ala His Arg Val Leu Phe Gly Phe Val Pro Glu Thr Lys Glu Glu Leu
 1 5 10 15
 Gln Val Met Pro Gly Asn Ile Val Phe Val Leu Lys Lys Gly Asn Asp
 20 25 30
 Ala Thr Val Met Phe Asn Gly Gln Lys
 35 40

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Arg Gly Ile Val Gln Tyr Asp Phe Met Ala Glu Ser Gln Asp Glu Leu
 1 5 10 15
 Thr Ile Lys Ser Gly Asp Lys Val Tyr Ile Leu Asp Asp Lys Lys Ser
 20 25 30

Lys Asp Met Cys Gln Leu Val Asp Ser Gly Lys
35 40

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Gln Ala Leu Phe Asp Pro Asp Pro Gln Glu Asp Gly Glu Leu Gly Phe
1 5 10 15

Arg Arg Gly Asp Phe Ile His Val Met Asp Asn Ser Asp Pro Asn Lys
20 25 30

Gly Ala Cys His Gly Gln
35

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Gln Ala Leu Tyr Pro Phe Ser Ser Ser Asn Asp Glu Glu Leu Asn Phe
1 5 10 15

Glu Lys Gly Asp Val Met Asp Val Ile Glu Lys Pro Glu Asn Asp Pro
20 25 30

Glu Lys Cys Arg Lys Ile Asn Gly Met
35 40

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Val Ala Met Tyr Asp Phe Gln Ala Thr Glu Ala His Asp Leu Arg Leu
1 5 10 15

Glu Arg Gly Gln Glu Tyr Ile Ile Leu Glu Lys Asn Asp Leu His Arg
20 25 30

Ala Arg Asp Lys Tyr Gly Trp

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Val	Ala	Leu	Tyr	Asp	Tyr	Asn	Pro	Met	Asn	Ala	Asn	Asp	Leu	Gln	Leu
1				5				10						15	

Arg	Lys	Gly	Asp	Glu	Tyr	Phe	Ile	Leu	Glu	Glu	Ser	Asn	Leu	Pro	Arg
				20				25					30		

Ala	Arg	Asp	Lys	Asn	Gly	Gln									
				35											

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Val	Ala	Leu	Tyr	Asp	Phe	Val	Ala	Ser	Gly	Asp	Asn	Thr	Leu	Ser	Ile
1				5				10					15		

Thr	Lys	Gly	Glu	Lys	Leu	Arg	Val	Leu	Gly	Tyr	Asn	His	Asn	Gly	Glu
				20				25				30			

Glu	Ala	Gln	Thr	Lys	Asn	Gly	Gln								
				35			40								

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Val	Ala	Leu	Tyr	Asp	Tyr	Glu	Ser	Arg	Thr	Glu	Thr	Asp	Leu	Ser	Phe
1				5				10					15		

Lys	Lys	Gly	Glu	Arg	Leu	Gln	Ile	Val	Asn	Asn	Thr	Glu	Gly	Asp	Leu
				20				25				30			

Ala	His	Ser	Leu	Ser	Thr	Gly	Gln								
				35			40								

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu Thr Phe
1 5 10 15
Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly Asp Glu
20 25 30
Ala Arg Ser Leu Ser Ser Gly Lys
35 40

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu Ser Phe
1 5 10 15
His Lys Gly Glu Lys Phe Gln Ile Leu Asn Ser Ser Glu Gly Asp Glu
20 25 30
Ala Arg Ser Leu Thr Thr Gly Glu
35 40

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe
1 5 10 15
Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Glu
20 25 30
Ala Arg Ser Ile Ala Thr Gly Lys
35 40

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Gly Asp Asp Leu Thr Phe
1 5 10 15
Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Tyr Asp Glu
20 25 30
Ala Arg Ser Leu Ser Ser Gly His
35 40

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Val Ala Leu Tyr Asp Tyr Glu Ala Arg Ile Ser Glu Asp Leu Ser Phe
1 5 10 15
Lys Lys Gly Glu Arg Leu Gln Ile Ile Asn Thr Ala Asp Gly Asp Tyr
20 25 30
Ala Arg Ser Leu Ile Thr Asn Ser
35 40

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Val Ala Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu Ser Phe
1 5 10 15
Gln Lys Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu Lys Ala
20 25 30
Arg Ser Leu Ala Thr Arg Lys
35

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp Asp Leu Ser Phe
1 5 10 15
Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His Gly Glu Lys Ala
20 25 30
Lys Ser Leu Leu Thr Lys Lys
35

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Val Ala Leu Pro Asp Tyr Ala Ala Val Asn Asp Arg Asp Leu Gln Val
1 5 10 15
Leu Lys Gly Glu Lys Leu Gln Val Leu Arg Ser Thr Gly Asp Leu Ala
20 25 30
Arg Ser Leu Val Thr Gly Arg
35

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu Gly Phe
1 5 10 15
Glu Lys Gly Glu Gln Leu Arg Ile Leu Glu Gln Ser Gly Glu Lys Ala
20 25 30
Gln Ser Leu Thr Thr Gly Gln
35

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Val Ala Lys Phe Asp Tyr Val Ala Gln Gln Glu Gln Glu Leu Asp Ile
1 5 10 15
Lys Lys Asn Glu Arg Leu Trp Leu Leu Asp Asp Ser Lys Ser Trp Val
20 25 30
Arg Asn Ser Met Asn Lys
35

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Arg Ala Ile Tyr Asp Tyr Glu Gln Val Gln Asn Ala Asp Glu Glu Leu
1 5 10 15
Thr Phe His Glu Asn Asp Val Phe Asp Val Phe Asp Asp Lys Asp Ala
20 25 30
Asp Leu Val Lys Ser Thr Val Ser Asn Glu
35 40

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Val Ala Leu Tyr Asp Tyr Gln Gly Glu Gly Ser Asp Glu Leu Ser Phe
1 5 10 15
Asp Pro Asp Asp Val Ile Thr Asp Ile Glu Met Val Asp Glu Gly Arg
20 25 30
Gly Arg Cys His Gly His
35

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 40 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Thr Ala Glu Tyr Asp Tyr Asp Ala Ala Glu Asp Asn Glu Leu Thr Phe
1 5 10 15

Val Glu Asn Asp Lys Ile Ile Asn Ile Glu Phe Val Asp Asp Asp Leu
20 25 30

Gly Glu Leu Glu Lys Asp Gly Ser
35 40

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Tyr Val Lys Phe Asn Tyr Asn Ala Glu Arg Glu Asp Glu Leu Ser Leu
1 5 10 15

Ile Lys Gly Thr Lys Val Ile Val Met Glu Lys Cys Ser Asp Gly Arg
20 25 30

Gly Ser Tyr Asn Gly Gln
35

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Lys Ala Arg Tyr Asp Phe Cys Ala Arg Asp Arg Ser Glu Leu Ser Leu
1 5 10 15

Lys Glu Gly Asp Ile Ile Lys Ile Leu Asn Lys Lys Gly Gln Gln Trp
20 25 30

Arg Gly Glu Ile Tyr Gly Arg
35

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Ile Ala Lys Tyr Asp Phe Lys Ala Thr Ala Asp Asp Glu Leu Ser Phe
1 5 10 15
Lys Arg Gly Asp Ile Leu Lys Val Leu Asn Glu Glu Cys Asp Gln Tyr
20 25 30
Lys Ala Glu Leu Asn Gly Lys
35

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Lys Ala Leu Tyr Asp Tyr Lys Ala Lys Arg Ser Asp Glu Leu Ser Phe
1 5 10 15
Cys Arg Gly Ala Leu Ile His Asn Val Ser Lys Glu Pro Gly Trp Lys
20 25 30
Gly Asp Tyr Gly Thr Arg Ile
35

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Lys Ala Leu Phe Asp Tyr Lys Ala Gln Arg Glu Asp Glu Leu Thr Phe
1 5 10 15
Ile Lys Ser Ala Ile Ile Gln Asn Val Glu Lys Gln Glu Gly Trp Arg
20 25 30
Gly Asp Tyr Gly Gly Lys Lys
35

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Lys Ala Leu Tyr Asp Tyr Asp Ala Gln Thr Gly Asp Glu Leu Thr Phe
1 5 10 15

Lys Glu Gly Asp Thr Ile Ile Val His Gln Lys Asp Pro Ala Trp Glu
20 25 30

Gly Glu Leu Asn Gly Lys
35

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Arg Ala Leu Tyr Asp Phe Ala Ala Glu Asn Pro Asp Glu Leu Thr Phe
1 5 10 15

Asn Glu Gly Ala Val Val Thr Val Ile Asn Lys Ser Asn Pro Trp Glu
20 25 30

Gly Glu Leu Asn Gly Gln
35

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Lys Ala Leu Tyr Asp Tyr Asp Ala Ser Ser Thr Asp Glu Leu Ser Phe
1 5 10 15

Lys Glu Gly Asp Ile Ile Phe Ile Val Gln Lys Asp Asn Gly Thr Gln
20 25 30

Gly Glu Leu Lys Ser Gly Gln
35

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Glu Ala Leu Phe Ser Tyr Glu Ala Thr Gln Pro Glu Asp Leu Glu Phe
1 5 10 15

Gln Glu Gly Asp Ile Ile Leu Val Leu Ser Lys Val Asn Glu Leu Glu
20 25 30

Gly Glu Cys Lys Gly Lys
35

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Arg Ala Ile Ala Asp Tyr Glu Lys Thr Ser Gly Ser Glu Met Ala Leu
1 5 10 15

Ser Thr Gly Asp Val Val Glu Val Val Glu Lys Ser Glu Ser Gly Phe
20 25 30

Cys Gln Met Lys Ala Lys
35

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Met Ala Leu Val Asp Phe Gln Ala Arg Ser Pro Arg Glu Val Thr Met
1 5 10 15

Lys Lys Gly Asp Val Leu Thr Leu Leu Ser Ser Ile Asn Lys Asp Lys
20 25 30

Val Glu Ala Ala Asp His
35

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Tyr Ala Ile Val Leu Tyr Asp Phe Lys Ala Glu Lys Ala Asp Glu Leu
1 5 10 15
Thr Thr Tyr Val Gly Glu Asn Leu Phe Ile Cys Ala His His Asn Cys
20 25 30
Glu Ile Ala Lys Pro Ile Gly Arg Leu Gly Gly
35 40

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Val Ala Ala Tyr Asp Phe Asn Tyr Pro Ile Lys Lys Asp Ser Ser Ser
1 5 10 15
Gln Leu Leu Ser Val Gln Gln Gly Glu Thr Ile Tyr Ile Leu Asn Lys
20 25 30
Asn Ser Ser Gly Asp Gly Leu Val Ile Asp Asp
35 40

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Arg Phe Gln Thr Thr Ala Ile Ser Asp Tyr Glu Asn Ser Ser Asn
1 5 10 15
Pro Ser Phe Leu Lys Phe Ser Ala Gly Asp Thr Ile Ile Val Ile Glu
20 25 30
Val Leu Glu Asp Cys Asp Gly
35

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Arg Ala Leu Val Asp Tyr Lys Lys Glu Arg Glu Glu Asp Ile Asp Leu
1 5 10 15

His Leu Gly Asp Ile Leu Thr Val Asn Lys Gly Ser Leu Val Ala Leu
20 25 30

Gly Phe Ser Asp Gly Gln Glu Ala Arg Pro Glu Glu Ile Leu Asn Gly
35 40 45

Tyr Asn Glu Thr Thr Gly Glu
50 55

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Asn Lys Gly Thr Val Tyr Ala Leu Trp Asp Tyr Glu Ala Gln Asn Ser
1 5 10 15

Asp Glu Leu Ser Phe His Glu Gly Asp Ala Ile Thr Ile Leu Arg Arg
20 25 30

Lys Asp Glu Asn Glu Thr Glu Trp Trp Trp Ala Arg Leu Gly Asp Arg
35 40 45

Glu Gly Tyr Val Pro Lys Asn Leu Leu Gly Leu Tyr
50 55 60

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Gln Val Lys Val Phe Arg Ala Leu Tyr Thr Phe Glu Pro Arg Thr Pro
1 5 10 15

Asp Glu Leu Tyr Phe Glu Glu Gly Asp Ile Ile Tyr Ile Thr Asp Met
20 25 30

Ser Asp Thr Ser Trp Trp Lys Gly Thr Cys Lys Gly Arg Thr Gly Leu
35 40 45

Ile Pro Ser Asn Tyr Val Ala Glu Gln
50 55

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

His Trp Thr Pro Tyr Arg Ala Met Tyr Gln Tyr Arg Pro Gln Asn Glu
1 5 10 15

Asp Glu Leu Glu Leu Arg Glu Gly Asp Arg Val Asp Val Met Gln Gln
20 25 30

Cys Asp Asp Gly Trp Phe Val Gly Val Ser Arg Arg Thr Gln Lys Phe
35 40 45

Gly Thr Phe Pro Gly Asn Tyr Val Ala Pro Val
50 55

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Asp Gln Pro Ser Cys Lys Ala Leu Tyr Asp Phe Glu Pro Glu Asn Asp
1 5 10 15

Gly Glu Leu Gly Phe Arg Glu Gly Asp Leu Ile Thr Leu Thr Asn Gln
20 25 30

Ile Asp Glu Asn Trp Tyr Glu Gly Met Leu His Gly Gln Ser Gly Phe
35 40 45

Phe Pro Leu Ser Tyr Val Gln Val Leu
50 55

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Leu Gly Ile Thr Ala Ile Ala Leu Tyr Asp Tyr Gln Ala Ala Gly Asp
1 5 10 15

Asp Glu Ile Ser Phe Asp Pro Asp Asp Ile Ile Thr Asn Ile Glu Met
20 25 30

Ile Asp Asp Gly Trp Trp Arg Gly Val Cys Lys Gly Arg Tyr Gly Leu
35 40 45

Phe Pro Ala Asn Tyr Val Glu Leu Arg
50 55

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Gly Gly Lys Arg Tyr Arg Ala Val Tyr Asp Tyr Ser Ala Ala Asp Glu
1 5 10 15

Asp Glu Val Ser Phe Gln Asp Gly Asp Thr Ile Val Asn Val Gln Gln
20 25 30

Ile Asp Asp Gly Trp Met Tyr Gly Thr Val Glu Arg Thr Gly Asp Thr
35 40 45

Gly Met Leu Pro Ala Asn Tyr Val Glu Ala Ile
50 55

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Gln Gly Leu Cys Ala Arg Ala Leu Tyr Asp Tyr Gln Ala Ala Asp Asp
1 5 10 15

Thr Glu Ile Ser Phe Asp Pro Glu Asn Leu Ile Thr Gly Ile Glu Val
20 25 30

Ile Asp Glu Gly Trp Trp Arg Gly Tyr Gly Pro Asp Gly His Phe Gly
35 40 45

Met Phe Pro Ala Asn Tyr Val Glu Leu Ile
50 55

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Asp Gln Pro Cys Cys Arg Ala Leu Tyr Asp Leu Glu Pro Glu Asn Glu

1	5	10	15												
Gly	Glu	Leu	Ala	Phe	Lys	Glu	Gly	Asp	Ile	Ile	Thr	Leu	Thr	Asn	Gln
				20				25						30	
Ile	Asp	Glu	Asn	Trp	Tyr	Glu	Gly	Met	Leu	His	Gly	Gln	Ser	Gly	Phe
				35				40				45			
Phe	Pro	Ile	Asn	Tyr	Val	Glu	Ile	Leu							
				50			55								

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Phe	Met	Phe	Lys	Val	Gln	Ala	Gln	His	Asp	Tyr	Thr	Ala	Thr	Asp	Thr
1				5				10						15	
Asp	Glu	Leu	Gln	Leu	Lys	Ala	Gly	Asp	Val	Val	Leu	Val	Ile	Pro	Phe
				20				25					30		
Gln	Asn	Pro	Glu	Glu	Gln	Asp	Glu	Gly	Trp	Leu	Met	Gly	Val	Lys	Glu
				35				40				45			
Ser	Asp	Trp	Asn	Gln	His	Lys	Glu	Leu	Glu	Lys	Cys	Arg	Gly	Val	Phe
				50				55			60				
Pro	Glu	Asn	Phe	Thr	Glu	Arg	Val								
				65			70								

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Phe	Met	Lys	Lys	Val	Gln	Ala	Gln	His	Asp	Tyr	Thr	Ala	Thr	Asp	Thr
1				5				10						15	
Asp	Glu	Leu	Gln	Leu	Lys	Ala	Gly	Asp	Val	Val	Leu	Val	Ile	Pro	Phe
				20				25					30		
Gln	Asn	Pro	Glu	Glu	Gln	Asp	Glu	Gly	Trp	Leu	Met	Gly	Val	Lys	Glu
				35				40				45			
Ser	Asp	Trp	Asn	Gln	His	Lys	Glu	Leu	Glu	Lys	Cys	Arg	Gly	Val	Phe
				50				55			60				
Pro	Glu	Asn	Phe	Thr	Glu	Arg	Val								
				65			70								

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ala Gly Ile Ser Ala Ile Ala Leu Tyr Asp Tyr Gln Gly Glu Gly Ser
1 5 10 15

Asp Glu Leu Ser Phe Asp Pro Asp Asp Ile Ile Thr Asp Ile Glu Met
20 25 30

Val Asp Glu Gly Trp Trp Arg Gly Gln Cys Arg Gly His Phe Gly Leu
35 40 45

Phe Pro Ala Asn Tyr Val Lys Leu Leu
50 55

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Glu Ala Glu Tyr Val Arg Ala Leu Phe Asp Phe Asn Gly Asn Asp Glu
1 5 10 15

Glu Asp Leu Pro Phe Lys Lys Gly Asp Ile Leu Arg Ile Arg Asp Lys
20 25 30

Pro Glu Glu Gln Trp Trp Asn Ala Glu Asp Ser Glu Gly Lys Arg Gly
35 40 45

Met Ile Pro Val Pro Tyr Val Glu Lys Tyr
50 55

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Arg Val Ile Gln Lys Arg Val Pro Asn Ala Tyr Asp Lys Thr Ala Leu
1 5 10 15

Ala Leu Glu Val Gly Glu Leu Val Lys Val Thr Lys Ile Asn Val Ser
20 25 30

Gly Gln Trp Glu Gly Glu Cys Asn Gly Lys Arg Gly His Phe Pro Phe
35 40 45
Thr His Val Arg Leu Leu
50

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Glu Met Arg Pro Ala Arg Ala Lys Phe Asp Phe Lys Ala Gln Thr Leu
1 5 10 15
Lys Glu Leu Pro Leu Gln Lys Gly Asp Val Val Tyr Ile Tyr Arg Gln
20 25 30
Ile Asp Gln Asn Trp Tyr Glu Gly Glu His His Gly Arg Val Gly Ile
35 40 45
Phe Pro Arg Thr Tyr Ile Glu Leu Leu
50 55

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Glu Tyr Gly Glu Ala Ile Ala Lys Phe Asn Phe Asn Gly Asp Thr Gln
1 5 10 15
Val Glu Met Ser Phe Arg Lys Gly Glu Arg Ile Thr Leu Leu Arg Gln
20 25 30
Val Asp Glu Asn Trp Tyr Glu Gly Arg Ile Pro Gly Thr Ser Arg Gln
35 40 45
Gly Ile Phe Pro Ile Thr Tyr Val Asp Val Leu
50 55

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Asp Leu Cys Ser Tyr Gln Ala Leu Tyr Ser Tyr Val Pro Gln Asn Asp
1 5 10 15
Asp Glu Leu Glu Leu Arg Asp Gly Asp Ile Val Asp Val Met Glu Lys
20 25 30
Cys Asp Asp Gly Trp Phe Val Gly Thr Ser Arg Arg Thr Arg Gln Phe
35 40 45
Gly Thr Phe Pro Gly Asn Tyr Val Lys Pro Leu
50 55

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Asp Gln Pro Cys Cys Arg Gly Leu Tyr Asp Phe Glu Pro Glu Asn Glu
1 5 10 15
Gly Glu Leu Gly Phe Lys Glu Gly Asp Ile Ile Thr Leu Thr Asn Gln
20 25 30
Ile Asp Glu Asn Trp Tyr Glu Gly Met Leu Arg Gly Glu Ser Gly Phe
35 40 45
Phe Pro Ile Asn Tyr Val Glu Val Ile
50 55

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Thr Glu Val Arg Val Arg Ala Leu Tyr Asp Tyr Glu Gly Gln Glu His
1 5 10 15
Asp Glu Leu Ser Phe Lys Ala Gly Asp Glu Leu Thr Lys Met Glu Asp
20 25 30
Glu Asp Glu Gln Gly Trp Cys Lys Gly Arg Leu Asp Asn Gly Gln Val
35 40 45
Gln Leu Tyr Pro Ala Asn Tyr Val Glu Ala Ile
50 55

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Lys Gly Val Arg Val Arg Ala Leu Tyr Asp Tyr Asp Gly Gln Glu Gln
1 5 10 15
Asp Glu Leu Ser Phe Lys Ala Gly Asp Glu Leu Thr Lys Leu Gly Glu
20 25 30
Glu Asp Glu Gln Gly Trp Cys Arg Gly Arg Leu Asp Ser Gly Gln Leu
35 40 45
Gly Leu Tyr Pro Ala Asn Tyr Val Glu Ala Ile
50 55

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Gln Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro
1 5 10 15
Asp Asp Leu Ser Phe Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu
20 25 30
His Gly Glu Trp Trp Lys Ala Lys Ser Leu Leu Thr Lys Lys Glu Gly
35 40 45
Phe Ile Pro Ser Asn Tyr Val Ala Lys Leu
50 55

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu
1 5 10 15
Asp Asp Leu Ser Phe His Lys Gly Glu Lys Phe Gln Ile Leu Asn Ser
20 25 30
Ser Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Thr Thr Gly Glu Thr

35

40

45

Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val
50 55

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Lys Val Val Tyr Tyr Arg Ala Leu Tyr Pro Phe Glu Ser Arg Ser His
1 5 10 15

Asp Glu Ile Thr Ile Gln Pro Gly Asp Ile Val Met Val Asp Glu Ser
20 25 30

Gln Thr Gly Glu Pro Gly Trp Leu Gly Gly Glu Leu Lys Gly Lys Thr
35 40 45

Gly Trp Phe Pro Ala Asn Tyr Ala Glu Lys Ile
50 55

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Glu Gly Leu Gln Ala Gln Ala Leu Tyr Pro Trp Arg Ala Lys Lys Asp
1 5 10 15

Asn His Leu Asn Phe Asn Lys Asn Asp Val Ile Thr Val Leu Glu Gln
20 25 30

Gln Asp Met Trp Trp Phe Gly Glu Val Gln Gly Gln Lys Gly Trp Phe
35 40 45

Pro Lys Ser Tyr Val Lys Leu Ile
50 55

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Gly Glu Glu Ile Ala Gln Val Ile Ala Ser Tyr Thr Ala Thr Gly Pro
 1 5 10 15

Glu Gln Leu Thr Leu Ala Pro Gly Gln Leu Ile Leu Ile Arg Lys Lys
 20 25 30

Asn Pro Gly Gly Trp Trp Glu Gly Glu Leu Gln Ala Arg Gly Lys Lys
 35 40 45

Arg Gln Ile Gly Trp Phe Pro Ala Asn Tyr Val Lys Leu Leu
 50 55 60

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Ala Val Cys Gln Val Ile Ala Met Tyr Asp Tyr Thr Ala Gln Asn Asp
 1 5 10 15

Asp Glu Leu Ala Phe Asn Lys Gly Gln Ile Ile Asn Val Leu Asn Lys
 20 25 30

Glu Asp Pro Asp Trp Trp Lys Gly Glu Val Asn Gly Gln Val Gly Leu
 35 40 45

Phe Pro Ser Asn Tyr Val Lys Leu Thr
 50 55

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Val Gly Glu Glu Tyr Ile Ala Leu Tyr Pro Tyr Ser Ser Val Glu Pro
 1 5 10 15

Gly Asp Leu Thr Phe Thr Glu Gly Glu Glu Ile Leu Val Thr Gln Lys
 20 25 30

Asp Gly Glu Trp Trp Thr Gly Ser Ile Gly Asp Arg Ser Gly Ile Phe
 35 40 45

Pro Ser Asn Tyr Val Lys Pro Lys
 50 55

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Lys	Pro	Glu	Ile	Ala	Gln	Val	Thr	Ser	Ala	Tyr	Val	Ala	Ser	Gly	Ser
1		5						10					15		
Glu	Gln	Leu	Ser	Leu	Ala	Pro	Gly	Gln	Leu	Ile	Leu	Ile	Leu	Lys	Lys
	20							25					30		
Asn	Thr	Ser	Gly	Trp	Trp	Gln	Gly	Glu	Leu	Gln	Ala	Arg	Gly	Lys	Lys
	35					40					45				
Arg	Gln	Lys	Gly	Trp	Phe	Pro	Ala	Ser	Tyr	Val	Lys	Leu	Leu		
	50				55					60					

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Pro	Val	Cys	Gln	Val	Ile	Gly	Met	Tyr	Asp	Tyr	Ala	Ala	Asn	Asn	Glu
1		5						10					15		
Asp	Glu	Leu	Ser	Phe	Ser	Lys	Gly	Gln	Leu	Ile	Asn	Val	Met	Asn	Lys
	20					25					30				
Asp	Asp	Pro	Asp	Trp	Trp	Gln	Gly	Glu	Ile	Asn	Gly	Val	Thr	Gly	Leu
	35					40				45					
Phe	Pro	Ser	Asn	Tyr	Val	Leu	Glu	Glu							
	50					55									

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Gly	Val	Thr	Thr	Phe	Val	Ala	Leu	Tyr	Asp	Tyr	Glu	Ser	Arg	Thr	Glu
1		5						10					15		
Thr	Asp	Leu	Ser	Phe	Lys	Lys	Gly	Glu	Arg	Leu	Gln	Ile	Val	Asn	Asn
	20				25						30				
Thr	Glu	Gly	Asp	Trp	Trp	Leu	Ala	His	Ser	Leu	Thr	Thr	Gly	Gln	Thr
	35				40						45				

Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser
50 55

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Pro Gly Thr Pro Pro Pro Pro Tyr Thr Val Gly Pro Gly Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

His Gly Pro Thr Pro Pro Pro Pro Tyr Thr Val Gly Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Tyr Val Gln Pro Pro Pro Pro Tyr Pro Gly Pro Met
1 5 10

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Pro Gly Tyr Pro Tyr Pro Pro Pro Pro Glu Phe Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Pro Gly Thr Pro Ala Pro Pro Tyr Thr Val Gly Pro Gly Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Pro Gly Thr Pro Pro Ala Pro Tyr Thr Val Gly Pro Gly Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Asp Ser Gly Val Arg Pro Leu Pro Pro Leu Pro Asp Pro Gly Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Val Arg Pro Leu Pro Pro Leu Pro Glu Glu Leu Pro Arg Pro Arg Arg
1 5 10 15

Pro Pro Pro Glu Asp
20

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Pro Pro Pro Ala Leu Pro Pro Pro Pro Arg Pro Val Ala Asp Lys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Ala Pro Ala Pro Pro Pro Gly Pro Pro Arg Pro Ala Ala Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Gly Gly Gly Phe Pro Pro Leu Pro Pro Pro Pro Tyr Leu Pro Pro Leu
1 5 10 15

Gly

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Ser Ile Ser Pro Arg Pro Arg Pro Pro Gly Arg Pro Val Ser Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Pro Pro Pro Glu His Ile Pro Pro Pro Pro Arg Pro Lys Arg Ile Leu
1 5 10 15

Glu

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Lys Glu Gly Glu Arg Ala Leu Pro Ser Ile Pro Lys Leu Ala Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Ser Arg Leu Lys Pro Ala Pro Pro Pro Pro Ala Ala Ser Ala Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Gln Ala Ser Leu Pro Pro Val Pro Pro Arg Asp Leu Leu Leu Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro Pro Pro Pro Pro Asp
1 5 10 15
Arg Pro Tyr Ser
20

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Ser Asp Gln Gly Arg Asn Leu Pro Gly Thr Pro Val Pro Ala Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Arg His Ser Arg Arg Gln Leu Pro Pro Val Pro Pro Lys Pro Arg Pro
1 5 10 15
Leu Leu

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Glu Lys Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met

1

5

10

15

Thr Tyr

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Pro Gln Pro His Arg Val Leu Pro Thr Ser Pro Ser Asp Ile Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Ala Asp Phe Gln Pro Pro Tyr Phe Pro Pro Pro Tyr Gln Pro Ile Tyr
1 5 10 15

Pro Gln Ser

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Ser Ser Ala Ala Pro Pro Pro Pro Arg Arg Ala Thr Pro Glu Lys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Ser Lys Lys Gly Val Met Thr Ala Pro Pro Pro Pro Pro Pro Pro Val
1 5 10 15
Tyr Glu Pro Gly Gly
20

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Glu Ala Phe Gln Pro Gln Glu Pro Asp Phe Pro Pro Pro Pro Pro Asp
1 5 10 15
Leu Glu

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Asp Glu Leu Ala Pro Pro Lys Pro Pro Leu Pro Glu Gly Glu Val Pro
1 5 10 15
Pro Pro Arg Pro Pro Pro Pro Glu
20

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Pro Gln Arg Arg Ala Pro Ala Val Pro Pro Ala Arg Pro Gly Ser Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Leu Gly Gly Ala Pro Pro Val Pro Ser Arg Pro Gly Ala Ser Pro Asp
1 5 10 15

Gly

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Pro Pro Pro Pro Leu Pro Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg
1 5 10 15

Gly Asn His

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Ala Ala Glu Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu Asp
1 5 10 15

Pro Gly Gly

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Asp Glu Glu Val Asn Ile Pro Pro His Thr Pro Val Arg Thr Val

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Ser Ala Glu Gly Asn Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg
1 5 10 15
Phe Asp

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Ala Trp Met Trp Gly Ser Pro Pro Glu Glu Glu Gly Trp Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Ala Glu Trp Leu Glu Gly Pro Pro Trp Tyr Asp Arg Lys Glu Gly Phe
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Gly Leu Glu Gly Trp Tyr Trp Glu Arg Gly Trp Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Trp Gly Leu Asp Gly Trp Leu Val Asp Gly Trp Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

Gly Ile Leu Ala Pro Pro Val Pro Pro Arg Asn Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Val Leu Lys Arg Pro Leu Pro Ile Pro Pro Val Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

Val Leu Lys Arg Pro Leu Pro Pro Leu Pro Val Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Ser Arg Ser Leu Ser Glu Val Ser Pro Lys Pro Pro Ile Arg Ser Val
1 5 10 15

Ser Leu Ser Arg
20

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Ser Arg Pro Pro Arg Trp Ser Pro Pro Pro Val Pro Leu Pro Thr Ser
1 5 10 15

Leu Asp Ser Arg
20

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Ser Arg Leu Gly Glu Phe Ser Lys Pro Pro Ile Pro Gln Lys Pro Thr
1 5 10 15

Trp Met Ser Arg
20

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Ser Phe Ala Ala Pro Ala Arg Pro Pro Val Pro Pro Arg Lys Ser Arg
1 5 10 15
Pro Gly Gly

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Ser Tyr Asp Ala Ser Ser Ala Pro Gln Arg Pro Pro Leu Pro Val Arg
1 5 10 15
Lys Ser Arg Pro Gly Gly
20

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Ser Pro Pro Pro Val Pro Pro Arg Pro Pro Ala Thr Leu Gly Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Ser Val Pro Ala Pro Pro Pro Leu Pro Pro Lys Ser Gly Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Ser Phe Ser Phe Pro Pro Leu Pro Pro Ala Pro Gly Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Ser Val Pro Leu Pro Pro Leu Arg Thr Val Ser Leu Gly Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1710 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

CACTCTCTAC ACTTGCACCG GCATCAAGGA CGAAAAGAAC GCGCTAGATA TGACTTGGAA	60
GCTGCTCAAG ACAATGAAC TACTTTCAAA GCTGGAGAAA TTATGACAGT TCTTGATGAC	120
AGTGATCCTA ACTGGTGGAA AGGTGAAACC CATCAAGGCA TAGGGTTATT TCCTTCTAAT	180
TTTGTGACTG CAGATCTCAC TGCTGAACCA GAAATGATTA AAACAGAGAA GAAGACGGTA	240
CAATTTAGTG ATGATGTTCA GGTAGAGACA ATAGAACCGAG AGCCGGAACCC AGCCTTTATT	300
GATGAAGATA AAATGGACCA GTTGCTACAG ATGCTGAAA GTACAGACCC CAGTGATGAT	360
CAGCCAGACC TACCAAGAGCT GCTTCATCTT GAAGCAATGT GTCACCAGAT GGGACCTCTC	420
ATTGATGAAA AGCTGGAAGA TATTGATAGA AAACATTCAAG AACTCTCAGA ACTTAATGTG	480
AAAGTGATGG AGGCCCTTTC CTTATATACC AAGTTAATGA ACGAAGATCC GATGTATTCC	540
ATGTATGCAA AGTTACAGAA TCAGCCATAT TATATGCAGT CATCTGGTGT TTCTGGTTCT	600
CAGGTGTATG CAGGGCCTCC TCCAAGTGGT GCCTACCTGG TTGCAGGGAA CGCGCAGATG	660
AGCCACCTCC AGAGCTACAG TCTTCCCCCG GAGCAGCTGT CTTCTCTCAG CCAGGCAGTG	720
GTCCCACCAT CCGCAAACCC AGCCCTTCCT AGTCAGCAGA CTCAGGCCGC TTACCCAAAC	780
CGCTCCCCAG GGGACCTCAT GAAGCCCGGT GATTCTGAAT GCCGTGGATC TGCCGAGGAT	840
TCCCAGATGC GTATTTCTCC TCCGTACTTC CCCACAGGAC AGCAGGCTTG AATAGCTGAT	900
TGCCTATGCA GGACAACAGG CTTGAATAGC TGACTGCCTA TGCATTCTCT TTGCTTGCCA	960

GT	TTTTTGGA	CATCAAAC	TTT GACAGATCCA	AGATTATTAC	TTTGATCTTC	CCCACACCCCC	1020		
CC	CCCC	GAGTCTACTA	TGGTCCCATC	ATAGTATTCT	GAAAATCAGT	GAATGGCCAC	1080		
T	TCTACCAGTT	ATTTCTACCA	GT	TTTAGGT	TCTAACCTC	AGGCATTCTG	GA	CTTCTG	1140
T	TTCATTATCA	TATTTGAAG	GCATTATCTT	CAAAATCTAT	CTAGACTCTG	ACCCTTCTC	1200		
C	CCATCTCCAC	CATTACTGCC	GTGGCTCTTC	TGCTGGTCGG	CTCTCTCCTG	GTGGATCCGT	1260		
A	AATAACCTGC	AGTCAGCTAT	CCTGGTCCAG	AAGGAAACCC	CGTTAAACCC	TGTTGGAATC	1320		
T	TTATCACGCT	TCTGCTCCAG	AACGAACCCA	GTCTGTCTGT	CTCACTCAGA	GTGTAAGCTA	1380		
C	CAGTCCTTAT	TGTGGCCATC	AGGTGCTGTG	TGTTCTCCAG	CCCCCTCCCC	ACCACCGCAG	1440		
C	CCCTGCCGGT	GATCTTAGCT	GCTCTCCCCT	CGGAACCCCC	TGCGGCCCCC	TCTGCCGCAA	1500		
A	CANTCGTGGC	CTGCTGTTCC	TTGAACATGC	TTGGTGT	TTCTCCTCAA	AGGCTTCTTT	1560		
N	CTGTTTACCT	GAAATGTACT	TGCCTAGGGA	AATCTTATCC	TGGCTCACTC	CGCTTACTTT	1620		
T	TTTCCACATC	TTTGCTAAA	GTTATTGCC	TTATTGGAGA	AGGCACCCCT	ACCATAAACT	1680		
T	AGAAATCCCT	TGCC	CCCAAG	CTGTTCC	TTT		1710		

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

His	Ser	Leu	His	Leu	His	Arg	His	Gln	Gly	Arg	Lys	Glu	Arg	Ala	Arg
1					5					10				15	

Tyr	Asp	Leu	Glu	Ala	Ala	Gln	Asp	Asn	Glu	Leu	Thr	Phe	Lys	Ala	Gly
				20				25				30			

Glu	Ile	Met	Thr	Val	Leu	Asp	Asp	Ser	Asp	Pro	Asn	Trp	Trp	Lys	Gly
		35					40				45				

Glu	Thr	His	Gln	Gly	Ile	Gly	Leu	Phe	Pro	Ser	Asn	Phe	Val	Thr	Ala
		50				55				60					

Asp	Leu	Thr	Ala	Glu	Pro	Glu	Met	Ile	Lys	Thr	Glu	Lys	Lys	Thr	Val
					65		70		75				80		

Gln	Phe	Ser	Asp	Asp	Val	Gln	Val	Glu	Thr	Ile	Glu	Pro	Glu	Pro	Glu
					85			90				95			

Pro	Ala	Phe	Ile	Asp	Glu	Asp	Lys	Met	Asp	Gln	Leu	Leu	Gln	Met	Leu
				100				105				110			

Gln	Ser	Thr	Asp	Pro	Ser	Asp	Asp	Gln	Pro	Asp	Leu	Pro	Glu	Leu	Leu
					115			120			125				

His	Leu	Glu	Ala	Met	Cys	His	Gln	Met	Gly	Pro	Leu	Ile	Asp	Glu	Lys
				130				135			140				

Leu	Glu	Asp	Ile	Asp	Arg	Lys	His	Ser	Glu	Leu	Ser	Glu	Leu	Asn	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

145	150	155	160
Lys Val Met Glu Ala Leu Ser Leu Tyr Thr Lys Leu Met Asn Glu Asp			
165	170	175	
Pro Met Tyr Ser Met Tyr Ala Lys Leu Gln Asn Gln Pro Tyr Tyr Met			
180	185	190	
Gln Ser Ser Gly Val Ser Gly Ser Gln Val Tyr Ala Gly Pro Pro Pro			
195	200	205	
Ser Gly Ala Tyr Leu Val Ala Gly Asn Ala Gln Met Ser His Leu Gln			
210	215	220	
Ser Tyr Ser Leu Pro Pro Glu Gln Leu Ser Ser Leu Ser Gln Ala Val			
225	230	235	240
Val Pro Pro Ser Ala Asn Pro Ala Leu Pro Ser Gln Gln Thr Gln Ala			
245	250	255	
Ala Tyr Pro Asn Arg Ser Pro Gly Asp Leu Met Lys Pro Gly Asp Ser			
260	265	270	
Glu Cys Arg Gly Ser Ala Glu Asp Ser Gln Met Arg Ile Ser Pro Pro			
275	280	285	
Tyr Phe Pro Thr Gly Gln Gln Ala			
290	295		

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1687 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAATTCTCGCGG CCGCGTCGAC CAAGGAGAGT GGCGCGTTCC AGGACGTGGG ACCCCAGGCC	60
CCAGTGGGCT CTGTGTACCA GAAGACCAAT GCCGTGTCAG AGATTTAAAG GGTTGGTTAG	120
ACAGCTTCTG GGCCAAAGCA GAGAAGGAGG AGGAGAACCG TCGGCTGGAG GAAAAGCGGT	180
GGGCCGAGGA GGCACAGCGG CAGCTGGAGC AGGAGCGCCG GGAGCGTGAG CTGCGTGAGG	240
CTGCACGCCG GGAGCAGCGC TATCAGGAGC AGGGTGGCGA GGCCAGCCCC CAGAGCAGGA	300
CGTGGGAGCA GCAGCAAGAA GTGGTTCAA GGAACCGAAA TGAGCAGGAG TCTGCCGTGC	360
ACCCGAGGGA GATTTCAAG CAGAAGGAGA GGGCCATGTC CACCACCTCC ATCTCCAGTC	420
CTCAGCCTGG CAAGCTGAGG AGCCCCTTCC TGCAGAAGCA GCTCACCCAA CCAGAGACCC	480
ACTTTGGCAG AGAGCCAGCT GCTGCCATCT CAAGGCCCAG GGCAGATCTC CCTGCTGAGG	540
AGCCGGCGCC CAGCACTCCT CCATGTCTGG TGCAGGCAGA AGAGGAGGCT GTGTATCAGG	600
AACCTCCAGA GCAGGAGACC TTCTACGAGC AGCCCCCACT GGTGCAGCAG CAAGGTGCTG	660
GCTCTGAGCA CATTGACCAAC CACATTCAGG GCCAGGGCT CAGTGGCAA GGGCTCTGTG	720
CCCGTGCCCT GTACGACTAC CAGGCAGCCC ACGACACAGA GATCTCCTTT GACCCCGAGA	780

ACCTCATCAC	GGGCATCGAG	GTGATCGACG	AAGGCTGGTG	GCGTGGCTAT	GGGCCGGATG	840
GCCATTTGG	CATGTTCCCT	GCCAATTACG	TGGAGCTCAT	TGATGAGGCT	GAGGGCACAT	900
CTTGCCTTC	CCCTCTCAGA	CATGGCTTC	TTATTGCTGG	AAGAGGAGGC	CTGGGAGTTG	960
ACATTCAGCA	CTCTTCCAGG	AATAGGACCC	CCAGTGAGGA	TGAGGCCTCA	GGGCTCCCTC	1020
CGGCTTGGCA	GACTCAGCCT	GTCACCCCAA	ATGCAGCAAT	GGCCTGGTGA	TTCCCACACA	1080
TCCCTCCTGC	ATCCCCCGAC	CCTCCCAGAC	AGCTTGGCTC	TTGCCCCTGA	CAGGATACTG	1140
AGCCAAGCCC	TGCCTGTGGC	CAAGCCCTGA	GTGGCCACTG	CCAAGCTGCG	GGGAAGGGTC	1200
CTGAGCAGGG	GCATCTGGGA	GGCTCTGGCT	GCCTCTGCA	TTTATTTGCC	TTTTTCTTT	1260
TTCTCTTGCT	TCTAAGGGGT	GGTGGCCACC	ACTGTTAGA	ATGACCCTTG	GGAACAGTGA	1320
ACGTAGAGAA	TTGTTTTAG	CAGAGTTGT	GACCAAAGTC	AGAGTGGATC	ATGGTGGTTT	1380
GGCAGCAGGG	AATTTGTCTT	GTTGGAGCCT	GCTCTGTGCT	CCCCACTCCA	TTTCTCTGTC	1440
CCTCTGCCTG	GGCTATGGGA	AGTGGGGATG	CAGATGCCA	AGCTCCCACC	CTGGGTATTG	1500
AAAAACGGCA	GACACAACAT	GTTCCTCCAC	GCGGCTCACT	CGATGCCTGC	AGGCCCCAGT	1560
GTGTGCCTCA	ACTGATTCTG	ACTTCAGGAA	AACTAACACA	GAGTGGCCTT	GGCCTGTTGT	1620
CTTCCCTAT	TTTCTGTCCC	AGTCATCCG	TGGTCGAAGC	GCCCGCGAAT	TCCAGCTGAG	1680
CGGGCGC						1687

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Ile	Arg	Gly	Arg	Val	Asp	Gln	Gly	Glu	Trp	Pro	Leu	Pro	Gly	Arg	Gly
1				5				10					15		
Thr	Pro	Gly	Pro	Ser	Gly	Leu	Cys	Val	Pro	Glu	Asp	Gln	Cys	Arg	Val
				20				25				30			
Arg	Asp	Leu	Lys	Gly	Trp	Leu	Asp	Ser	Phe	Trp	Ala	Lys	Ala	Glu	Lys
				35				40				45			
Glu	Glu	Glu	Asn	Arg	Arg	Leu	Glu	Glu	Lys	Arg	Trp	Ala	Glu	Glu	Ala
				50				55			60				
Gln	Arg	Gln	Leu	Glu	Gln	Glu	Arg	Arg	Glu	Arg	Glu	Leu	Arg	Glu	Ala
				65				70			75		80		
Ala	Arg	Arg	Glu	Gln	Arg	Tyr	Gln	Glu	Gln	Gly	Gly	Glu	Ala	Ser	Pro
				85				90				95			
Gln	Ser	Arg	Thr	Trp	Glu	Gln	Gln	Glu	Val	Val	Ser	Arg	Asn	Arg	
				100				105			110				
Asn	Glu	Gln	Glu	Ser	Ala	Val	His	Pro	Arg	Glu	Ile	Phe	Lys	Gln	Lys

115	120	125
Glu Arg Ala Met Ser Thr Thr Ser Ile Ser Ser Pro Gln Pro Gly Lys		
130 135 140		
Leu Arg Ser Pro Phe Leu Gln Lys Gln Leu Thr Gln Pro Glu Thr His		
145 150 155 160		
Phe Gly Arg Glu Pro Ala Ala Ala Ile Ser Arg Pro Arg Ala Asp Leu		
165 170 175		
Pro Ala Glu Glu Pro Ala Pro Ser Thr Pro Pro Cys Leu Val Gln Ala		
180 185 190		
Glu Glu Glu Ala Val Tyr Glu Glu Pro Pro Glu Gln Glu Thr Phe Tyr		
195 200 205		
Glu Gln Pro Pro Leu Val Gln Gln Gly Ala Gly Ser Glu His Ile		
210 215 220		
Asp His His Ile Gln Gly Gln Gly Leu Ser Gly Gln Gly Leu Cys Ala		
225 230 235 240		
Arg Ala Leu Tyr Asp Tyr Gln Ala Ala Asp Asp Thr Glu Ile Ser Phe		
245 250 255		
Asp Pro Glu Asn Leu Ile Thr Gly Ile Glu Val Ile Asp Glu Gly Trp		
260 265 270		
Trp Arg Gly Tyr Gly Pro Asp Gly His Phe Gly Met Phe Pro Ala Asn		
275 280 285		
Tyr Val Glu Leu Ile Asp Glu Ala Glu Gly Thr Ser Cys Pro Ser Pro		
290 295 300		
Leu Arg His Gly Phe Leu Ile Ala Gly Arg Gly Gly Leu Gly Val Asp		
305 310 315 320		
Ile Gln His Ser Ser Arg Asn Arg Thr Pro Ser Glu Asp Glu Ala Ser		
325 330 335		
Gly Leu Pro Pro Ala Trp Gln Thr Gln Pro Val Thr Pro Asn Ala Ala		
340 345 350		
Met Ala Trp		
355		

(2). INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2873 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

GC GGCCGCGT CGACATTGAA AGGAAAAGAT TAGAACTAAT GCAGAAAAAG AAACTAGAAG	60
ATGAGGCTGC AAGGAAAGCA AAGCAAGGAA AAGAAAACCTT ATGGAAAGAA AATCTTAGAA	120
AGGAGGAAGA AGAAAAACAA AAGCGACTCC AGGAAGAAAA AACACAAGAA AAAATTCAAG	180
AAGAGGAACG GAAAGCTGAG GAGAAACAAC GTGAGACAGC TAGTGTTC GTGAATTATA	240

GAGCATTATA	CCCCTTGAA	GCAAGGAACC	ATGATGAGAT	GAGTTTAAT	TCTGGAGATA	300
TAATTCAGGT	TGATGAAAAA	ACCGTAGGAG	AACCTGGTTG	GCTTTATGGT	AGTTTCAAG	360
GAAATTTGG	CTGGTTCCA	TGCAATTATG	TAGAAAAAAT	GCCATCAAGT	GAAAATGAAA	420
AAGCTGTATC	TCCAAAGAAG	GCCTTACTTC	CTCCTACAGT	TTCTTATCT	GCTACCTCAA	480
CTTCCTCTGA	ACCACTTCT	TCAAATCAAC	CAGCATCAGT	GAETGATTAT	CAAAATGTAT	540
CTTTTCAAA	CCTAACTCTA	AATACATCAT	GGCAGAAAAA	ATCAGCCTTC	ACTCGAACTG	600
TGTCCCCTGG	ATCTGTATCA	CCTATTCATG	GACAGGGACA	AGTGGTAGAA	AACTTAAAG	660
CACAGGCCCT	TTGTTCTGG	ACTGCAAAGA	AAGATAACCA	CTTGAACCTTC	TCAAAACATG	720
ACATTATTAC	TGTCTGGAG	CAGCAAGAAA	ATTGGTGGTT	TGGGGAGGTG	CATGGAGGAA	780
GAGGATGGTT	TCCCAAATCT	TATGTCAAGA	TCATTCTGG	GAGTGAAGTA	AAACGGGAAG	840
AACCAGAAGC	TTTGTATGCA	GCTGTAAATA	AGAAACCTAC	CTCGGCAGCC	TATTCAGTTG	900
GAGAAGAATA	TATTGCACTT	TATCCATATT	CAAGTGTGGA	ACCTGGAGAT	TTGACTTTCA	960
CAGAAGGTGA	AGAAATATTG	GTGACCCAGA	AAGATGGAGA	GTGGTGGACA	GGAAGTATTG	1020
GAGATAGAAG	TGGAATTTTT	CCATCAAAC	ATGTCAAACC	AAAGGATCAA	GAGAGTTTG	1080
GGAGTGCTAG	CAAGTCTGGA	GCATCAAATA	AAAAACCTGA	GATTGCTCAG	GTAACCTTCAG	1140
CATATGTTGC	TTCTGGTTCT	GAACAACTTA	GCCTTGCACC	AGGACAGTTA	ATATTAATTC	1200
TAAAGAAAAA	TACAAGTGGG	TGGTGGCAAG	GAGAGTTACA	GGCCAGAGGA	AAAAAGCGAC	1260
AGAAAGGATG	GTTCCTGCC	AGTCATGTTA	AACTTTGGG	TCCAAGTAGT	GAAAGAGCCA	1320
CACCTGCCTT	TCATCCTGTA	TGTCAGGTGA	TTGCTATGTA	TGACTATGCA	GCAAATAATG	1380
AAGATGAGCT	CAGTTCTCC	AAGGGACAAC	TCATTAATGT	TATGAACAAA	GATGATCCTG	1440
ATTGGTGGCA	AGGAGAGATC	AACGGGGTGA	CTGGTCTCTT	TCCTTCAAAAC	TACGTTAAGA	1500
TGACGACAGA	CTCAGATCCA	AGTCAACAGT	GACCCAATGT	TGTCTTCCAG	TTGTGAAAGC	1560
ACCCCGAGAGA	CCCACATATCC	AAGTTTCACT	CTAGCGTGG	GGCAGGGCAG	GCAGCCCTGA	1620
TCAAATATCT	CCTACACAAT	TCGTTTACTT	CGTTGAATG	TTAGAGCCAC	TTGTGATTAT	1680
TTTTTGTGT	TTCTAACTTA	CAGTTAAAT	TTATTGTAA	AAAGTTAAAG	GATAGTGGGT	1740
CTTGTGTGG	CTTCCCTGC	TGTTCACTCT	GGCATCTTA	GCATTTTCT	TCTTTTTAA	1800
TTTGATAATT	GTAGGTCAATT	AGCATGCATA	TTGAGTTGC	CCTTATGTGG	TGGGAGTTCA	1860
AACACACAAA	GACCCACTAT	TTGCACAAAC	TATTCTTACT	GGTTTGGAAAT	AGGCTGCCAT	1920
GCTTTTTAA	TGTTATTGCA	ACATGTGTAT	TCATTTACAG	AATTCAGATA	AAATTTGCTT	1980
ATGTTCTGCT	ATTATGTTG	ATCTAATCCT	AATCACAGTG	AGCTCTTAAT	TAGCTCAATA	2040
TGTGGTTTGC	CCTCAAGTGT	GCACGTGTTA	TTACTTTGTA	ATATGCCACT	ATGAGTACTG	2100
ACATTTAGAT	ATGTTAAAG	GCCAAGAACT	GGAAACAGCC	ATGCCCTGTT	TTCTGTGTAT	2160
TTGGGATGGG	AATAACAACA	TTTGGGGGG	AGCTTTTAA	ATCTCAGAGA	AGAGGAAAGT	2220
GGCCTGCTCT	GGCAGGTATG	TGCAGTGT	TTTGTCC	AGTCCCAAGA	ATGAGCACTG	2280

TCCTATGGTA GTTCGCTTAG GATCTTATG TGCTCTGGC TAATGAAGGT ACTGCATCAT	2340
GTGCTGCAGC GTGTGTATTC TTTTCGATG ACCTATAAAG GGATTATTT TGAGGAATGA	2400
AAGGCTCCA TCATTGACTG TGAGATGGGA AAAACCTTC CTAGCTTAGA GCATTTATAT	2460
CTTAATCCAT TTTAAAGTCA GAGTCATTG TTACCTGTT TAATCAGGTG ACTACATGTC	2520
CCAGTATACA AAGGGCACT GGGTGCACATT CTTCTTAATG TATTTAGTAA ATATCATAAG	2580
AAATCCTTTA AGAGTTAAA TGTCACAAA ACAGACATGC GGGCTCTAGT CAAGAATGAA	2640
TTAGAGTGAA GGAAAGCTGT GTAACACCTG GCATTCCTCT GTGTTCATGG AGCTCTTG	2700
AGGCTCTAAG ATTGATTTA CCATCAGACT TCTCTAATAC CTGTTCTCA ACCATATTGG	2760
CTACTTGAC ATAAGAATT ACTTCTTTC CTGGAATGGA AAACACTTTA AAAAATAATA	2820
ACAAACATTA TTATAAACTA ATATATGTGA GAGGTCGACG CGGCCGCGAA TTC	2873

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Gly Arg Val Asp Ile Glu Arg Lys Arg Leu Glu Leu Met Gln Lys Lys	
1 5 10 15	
Lys Leu Glu Asp Glu Ala Ala Arg Lys Ala Lys Gln Gly Lys Glu Asn	
20 25 30	
Leu Trp Lys Glu Asn Leu Arg Lys Glu Glu Glu Lys Gln Lys Arg	
35 40 45	
Leu Gln Glu Glu Lys Thr Gln Glu Lys Ile Gln Glu Glu Arg Lys	
50 55 60	
Ala Glu Glu Lys Gln Arg Glu Thr Ala Ser Val Leu Val Asn Tyr Arg	
65 70 75 80	
Ala Leu Tyr Pro Phe Glu Ala Arg Asn His Asp Glu Met Ser Phe Asn	
85 90 95	
Ser Gly Asp Ile Ile Gln Val Asp Glu Lys Thr Val Gly Glu Pro Gly	
100 105 110	
Trp Leu Tyr Gly Ser Phe Gln Gly Asn Phe Gly Trp Phe Pro Cys Asn	
115 120 125	
Tyr Val Glu Lys Met Pro Ser Ser Glu Asn Glu Lys Ala Val Ser Pro	
130 135 140	
Lys Lys Ala Leu Leu Pro Pro Thr Val Ser Leu Ser Ala Thr Ser Thr	
145 150 155 160	
Ser Ser Glu Pro Leu Ser Ser Asn Gln Pro Ala Ser Val Thr Asp Tyr	
165 170 175	
Gln Asn Val Ser Phe Ser Asn Leu Thr Val Asn Thr Ser Trp Gln Lys	

180

185

190

Lys Ser Ala Phe Thr Arg Thr Val Ser Pro Gly Ser Val Ser Pro Ile
 195 200 205
 His Gly Gln Gly Gln Val Val Glu Asn Leu Lys Ala Gln Ala Leu Cys
 210 215 220
 Ser Trp Thr Ala Lys Lys Asp Asn His Leu Asn Phe Ser Lys His Asp
 225 230 235 240
 Ile Ile Thr Val Leu Glu Gln Gln Glu Asn Trp Trp Phe Gly Glu Val
 245 250 255
 His Gly Gly Arg Gly Trp Phe Pro Lys Ser Tyr Val Lys Ile Ile Pro
 260 265 270
 Gly Ser Glu Val Lys Arg Glu Glu Pro Glu Ala Leu Tyr Ala Ala Val
 275 280 285
 Asn Lys Lys Pro Thr Ser Ala Ala Tyr Ser Val Gly Glu Glu Tyr Ile
 290 295 300
 Ala Leu Tyr Pro Tyr Ser Ser Val Glu Pro Gly Asp Leu Thr Phe Thr
 305 310 315 320
 Glu Gly Glu Glu Ile Leu Val Thr Gln Lys Asp Gly Glu Trp Trp Thr
 325 330 335
 Gly Ser Ile Gly Asp Arg Ser Gly Ile Phe Pro Ser Asn Tyr Val Lys
 340 345 350
 Pro Lys Asp Gln Glu Ser Phe Gly Ser Ala Ser Lys Ser Gly Ala Ser
 355 360 365
 Asn Lys Lys Pro Glu Ile Ala Gln Val Thr Ser Ala Tyr Val Ala Ser
 370 375 380
 Gly Ser Glu Gln Leu Ser Leu Ala Pro Gly Gln Leu Ile Leu Ile Leu
 385 390 395 400
 Lys Lys Asn Thr Ser Gly Trp Trp Gln Gly Glu Leu Gln Ala Arg Gly
 405 410 415
 Lys Lys Arg Gln Lys Gly Trp Phe Pro Ala Ser His Val Lys Leu Leu
 420 425 430
 Gly Pro Ser Ser Glu Arg Ala Thr Pro Ala Phe His Pro Val Cys Gln
 435 440 445
 Val Ile Ala Met Tyr Asp Tyr Ala Ala Asn Asn Glu Asp Glu Leu Ser
 450 455 460
 Phe Ser Lys Gly Gln Leu Ile Asn Val Met Asn Lys Asp Asp Pro Asp
 465 470 475 480
 Trp Trp Gln Gly Glu Ile Asn Gly Val Thr Gly Leu Phe Pro Ser Asn
 485 490 495
 Tyr Val Lys Met Thr Thr Asp Ser Asp Pro Ser Gln Gln
 500 505

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 543 bases

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

GAATTCTCGTCG	ACCCACCGCGT	CCGAAATATA	ACTGAAGTTG	GGGCACCTAC	TGAAGAAGAG	60
GAAGAAAAGTG	AAAGTGAAGA	TAGTGAAGAC	AGTGGTGGGG	AGGAAGAAGA	TGCAGAGGAG	120
GAAGAGGAAG	AGAAAGAGGA	AAATGAATCT	CACAAATGGT	CAACCGGTGA	AGAATACATC	180
GCTGTTGGAG	ATTTTACTGC	TCAGCAAGTT	GGAGATCTTA	CATTAAAGAA	AGGGGAAATT	240
CTCCTTGTAA	TTGAAAAAAA	ACCTGATGGT	TGGTGGATAG	CTAAGGATGC	CAAAGGAAAT	300
GAAGGTCTTG	TTCCCCAGAAC	CTACCTAGAG	CCTTATAGTG	AAGAAGAAGA	AGGCCAAGAG	360
TCAAGTGAAG	AGGGCAGTGA	AGAAGATGTA	GAGGCCGTGG	ATGAAACACGC	AGATGGAGCA	420
GAAGTTAACG	AAAGAACTGA	TCCCCACTGG	AGTGCTGTTC	AGAAAGCGAT	TTCAGAGGCG	480
GGCATCTTCT	GTCTTGTAA	TCATGTCTCG	TTTGCTACC	TAATAGTTCT	GATCCGTCCC	540
TAA						543

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Glu	Phe	Val	Asp	Pro	Arg	Val	Arg	Asn	Ile	Thr	Glu	Val	Gly	Ala	Pro
1				5					10					15	
Thr	Glu	Glu	Glu	Glu	Ser	Glu	Ser	Glu	Asp	Ser	Glu	Asp	Ser	Gly	
	20					25					30				
Gly	Glu	Glu	Glu	Asp	Ala	Glu	Glu	Glu	Glu	Lys	Glu	Glu	Asn		
	35				35		40			45					
Glu	Ser	His	Lys	Trp	Ser	Thr	Gly	Glu	Glu	Tyr	Ile	Ala	Val	Gly	Asp
	50				55					60					
Trp	Thr	Ala	Gln	Gln	Val	Gly	Asp	Leu	Thr	Phe	Lys	Lys	Gly	Glu	Ile
	65				70			75		80					
Leu	Leu	Val	Ile	Glu	Lys	Pro	Asp	Gly	Trp	Trp	Ile	Ala	Lys	Asp	
			85			90					95				
Ala	Lys	Gly	Asn	Glu	Gly	Leu	Val	Pro	Arg	Thr	Tyr	Leu	Glu	Pro	Tyr
	100					105					110				
Ser	Glu	Glu	Glu	Gly	Gln	Glu	Ser	Ser	Glu	Glu	Gly	Ser	Glu	Glu	
	115					120					125				
Asp	Val	Glu	Ala	Val	Asp	Glu	Thr	Ala	Asp	Gly	Ala	Glu	Val	Lys	Gln
	130				135					140					

Arg	Thr	Asp	Pro	His	Trp	Ser	Ala	Val	Gln	Lys	Ala	Ile	Ser	Glu	Ala
145					150				155					160	
Gly	Ile	Phe	Cys	Leu	Val	Asn	His	Val	Ser	Phe	Cys	Tyr	Leu	Ile	Val
				165				170					175		
Leu	Ile	Arg	Pro												
				180											

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 971 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

GAATTGGCG	GAATTGGCG	CCGCGTCGAC	GAAGAAACCT	GAAGGACACA	CTAGGCCTCG	60
GCAAGACGCG	CAGGAAGACC	AGCGCGCGGG	ATGCGTCCCC	CACGCCAGC	ACGGACGCCG	120
AGTACCCCGC	CAATGGCAGC	GGCGCCGACC	GCATCTACGA	CCTAACATC	CCGGCCTTCG	180
TCAAGTCGC	CTATGTGGCC	GAGCGGGAGG	ATGAGTTGTC	CCTGGTGAAG	GGGTCGCGCG	240
TCACCGTCAT	GGAGAAGTGC	AGCGACGGTT	GGTGGCGGGG	CAGCTACAAAC	GGGCAGATCG	300
GCTGGTTCCC	CTCCAACTAC	GTCTTGGAGG	AGGTGGACGA	GGCGGTTGCG	GAGTCCCCAA	360
GCTTCCTGAG	CCTGCGCAAG	GGCGCCTCGC	TGAGCAATGG	CCAGGGCTCC	CGCGTGCTGC	420
ATGTGGTCCA	GACGCTGTAC	CCCTTCAGCT	CAGTCACCGA	GGAGGAGCTC	AAGTTCGAGA	480
AGGGGGAGAC	CATGGAGGTG	ATTGAGAACG	CGGAGAACGA	CCCCGAGTGG	TGGAAATGCA	540
AAAATGCCCG	GGGCCAGGTG	GGCCTCGTCC	CCAAAAACTA	CGTGGTGGTC	CTCAGTGACG	600
GGCCTGCCCT	GCACCCCTGCG	CACGCCAAC	AGATAAGCTA	CACCGGGCCC	TCGTCGAGCG	660
GCGCTTCGCG	GGGCAGAGAG	TGGTACTACG	GGAACGTGAC	GCGGCACCAAG	GCCGAGTGCG	720
CCCTCAACGA	GGGGGGCGTG	GAGGGCGACT	TCCTCATTAG	GGACAGCGAG	TCCTCGCCCA	780
GCGACTTCTC	CGTGTCCCTT	AAAGCGTCAG	GGAAGAACAA	ACACTTCAAG	GTGCAGCTCG	840
TGGACAATGT	CTACTGCATT	GGGCAGCGGC	GCTTCCACAC	CATGGACCGAG	CTGGTGGAAC	900
ACTACAAAAAA	GGCGCCCATC	TTCACCAGCG	AGCACGGGA	GAAGCTCTAC	CTCGTCAGGG	960
CCCTGCAGTG A						971

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Ile Arg Arg Thr Ser Arg Pro Arg Arg Arg Asn Leu Lys Asp Thr
1 5 10 15

Leu Gly Leu Gly Lys Thr Arg Arg Lys Thr Ser Ala Arg Asp Ala Ser
20 25 30

Pro Thr Pro Ser Thr Asp Ala Glu Tyr Pro Ala Asn Gly Ser Gly Ala
35 40 45

Asp Arg Ile Tyr Asp Leu Asn Ile Pro Ala Phe Val Lys Phe Ala Tyr
50 55 60

Val Ala Glu Arg Glu Asp Glu Leu Ser Leu Val Lys Gly Ser Arg Val
65 70 75 80

Thr Val Met Glu Lys Cys Ser Asp Gly Trp Trp Arg Gly Ser Tyr Asn
85 90 95

Gly Gln Ile Gly Trp Phe Pro Ser Asn Tyr Val Leu Glu Glu Val Asp
100 105 110

Glu Ala Val Ala Glu Ser Pro Ser Phe Leu Ser Leu Arg Lys Gly Ala
115 120 125

Ser Leu Ser Asn Gly Gln Gly Ser Arg Val Leu His Val Val Gln Thr
130 135 140

Leu Tyr Pro Phe Ser Ser Val Thr Glu Glu Glu Leu Asn Phe Glu Lys
145 150 155 160

Gly Glu Thr Met Glu Val Ile Glu Lys Pro Glu Asn Asp Pro Glu Trp
165 170 175

Trp Lys Cys Lys Asn Ala Arg Gly Gln Val Gly Leu Val Pro Lys Asn
180 185 190

Tyr Val Val Val Leu Ser Asp Gly Pro Ala Leu His Pro Ala His Ala
195 200 205

Pro Gln Ile Ser Tyr Thr Gly Pro Ser Ser Ser Gly Arg Phe Ala Gly
210 215 220

Arg Glu Trp Tyr Tyr Gly Asn Val Thr Arg His Gln Ala Glu Cys Ala
225 230 235 240

Leu Asn Glu Arg Gly Val Glu Gly Asp Phe Leu Ile Arg Asp Ser Glu
245 250 255

Ser Ser Pro Ser Asp Phe Ser Val Ser Leu Lys Ala Ser Gly Lys Asn
260 265 270

Lys His Phe Lys Val Gln Leu Val Asp Asn Val Tyr Cys Ile Gly Gln
275 280 285

Arg Arg Phe His Thr Met Asp Glu Leu Val Glu His Tyr Lys Lys Ala
290 295 300

Pro Ile Phe Thr Ser Glu His Gly Glu Lys Leu Tyr Leu Val Arg Ala
305 310 315 320

Leu Gln

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GAATTCGCGG ACTTCGCGGC CGCGTCGACA CCAGTGCAGG TTTTGAATA TGGAGAAGCT	60
ATTGCTAAGT TTAACCTTAA TGGTGATACA CAAGTAGAAA TGTCCTTCAG AAAGGGTGAG	120
AGGATCACAC TGCTCCGGCA GGTAGATGAG AACTGGTACG AAGGGAGGAT CCCGGGGACA	180
TCCCGACAAG GCATCTTCCC CATCACCTAC GTGGATCTGA TCAAGCGACC ACTGGTGAAA	240
AACCCGTGG ATTACATGGA CCTGCCTTTC TCCTCCTCCC CAAGTCGCAG TGCCACTGCA	300
AGCCCACAGC AACCTCAAGC CCAGCAGCGA AGAGTCACCC CCGACAGGAG TCAAACCTCA	360
CAAGATTTAT TTAGCTATCA AGCATTATAT AGCTATATAC CACAGAATGA TGATGAGTTG	420
GAACCTCGCG ATGGAGATAT CGTTGATGTC ATGGAAAAT GTGACGATGG ATGGTTGTT	480
GGTACTTCAA GAAGGACAAA GCAGTTGGT ACTTTCCAG GCAACTATGT AAAACTTTG	540
TATCTATAA	549

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Glu Phe Ala Asp Phe Ala Ala Ala Ser Thr Pro Val Gln Val Leu Glu	
1 5 10 15	
Tyr Gly Glu Ala Ile Ala Lys Phe Asn Phe Asn Gly Asp Thr Gln Val	
20 25 30	
Glu Met Ser Phe Arg Lys Gly Glu Arg Ile Thr Leu Leu Arg Gln Val	
35 40 45	
Asp Glu Asn Trp Tyr Glu Gly Arg Ile Pro Gly Thr Ser Arg Gln Gly	
50 55 60	
Ile Phe Pro Ile Thr Tyr Val Asp Val Ile Lys Arg Pro Leu Val Lys	
65 70 75 80	
Asn Pro Val Asp Tyr Met Asp Leu Pro Phe Ser Ser Ser Pro Ser Arg	
85 90 95	
Ser Ala Thr Ala Ser Pro Gln Gln Pro Gln Ala Gln Gln Arg Arg Val	
100 105 110	
Thr Pro Gln Arg Ser Gln Thr Ser Gln Asp Leu Phe Ser Tyr Gln Ala	
115 120 125	

Leu Tyr Ser Tyr Ile Pro Gln Asn Asp Asp Glu Leu Glu Leu Arg Asp
 130 135 140
 Gly Asp Ile Val Asp Val Met Glu Lys Cys Asp Asp Gly Trp Phe Val
 145 150 155 160
 Gly Thr Ser Arg Arg Thr Lys Gln Phe Gly Thr Phe Pro Gly Asn Tyr
 165 170 175
 Val Lys Pro Leu Tyr Leu
 180

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Other
 - (D) OTHER INFORMATION: May or may not have carboxy-terminal amide and/or biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Ser Phe Ala Ala Pro Ala Arg Pro Pro Val Pro Pro Arg Lys Ser Arg
 1 5 10 15
 Pro Gly Gly

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Other
 - (D) OTHER INFORMATION: May or may not have carboxy-terminal amide and/or biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Ser Phe Ser Phe Pro Pro Leu Pro Pro Ala Pro Gly Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Ala Pro Pro Val Pro Pro Arg
1 5

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Gln Val Lys Val Phe Arg Ala Leu Tyr Thr Phe Glu Pro Arg Thr Pro
1 5 10 15

Asp Glu Leu Tyr Phe Glu Glu Gly Asp Ile Ile Tyr Ile Thr Asp Met
20 25 30

Asp Thr Asn Trp Trp Lys Gly Thr Ser Gly Arg Thr Gly Leu Ile Pro
35 40 45

Ser Asn Tyr Val Ala Glu Gln
50 55

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Thr Gly Glu Glu Tyr Ile Ala Val Gly Asp Phe Thr Ala Gln Gln Val
1 5 10 15

Gly Asp Leu Thr Phe Lys Lys Gly Glu Ile Leu Leu Val Ile Glu Lys
20 25 30

Lys Pro Asp Gly Trp Trp Ile Ala Lys Asp Ala Lys Gly Asn Glu Gly
35 40 45

Leu Val Pro Arg Thr Tyr Leu Glu Pro Tyr
50 55

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Tyr Leu Glu Lys Val Val Ala Ile Tyr Asp Tyr Thr Lys Asp Lys Glu
1 5 10 15

Asp Glu Leu Ser Phe Gln Glu Gly Ala Ile Ile Tyr Val Ile Lys Lys
20 25 30

Asn Asp Asp Gly Trp Tyr Glu Gly Val Met Asn Gly Thr Val Gly Leu
35 40 45

Ser Pro Gly Asn Tyr Val Glu Ser Ile
50 55

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Leu Asn Ile Pro Ala Phe Val Lys Phe Ala Tyr Val Ala Glu Arg Glu
1 5 10 15

Asp Glu Leu Ser Leu Val Lys Gly Ser Arg Val Thr Val Met Glu Lys
20 25 30

Cys Ser Asp Gly Trp Trp Arg Gly Ser Tyr Asn Gly Gln Ile Gly Trp
35 40 45

Phe Pro Ser Asn Tyr Val Leu Glu Glu
50 55

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Val Leu His Val Val Gln Thr Leu Tyr Pro Phe Ser Ser Val Thr Glu
1 5 10 15

Glu Glu Leu Asn Glu Phe Glu Lys Gly Glu Thr Met Glu Val Ile Glu
20 25 30

Lys Pro Glu Asn Asp Pro Glu Trp Trp Lys Cys Lys Asn Ala Arg Gly
35 40 45

Gln Val Gly Leu Val Pro Lys Asn Tyr Val Val Val Leu
50 55 60

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Glu	Glu	Val	Val	Val	Val	Ala	Lys	Phe	Asp	Tyr	Val	Ala	Gln	Gln	Glu
1					5				10						15
Gln	Glu	Leu	Asp	Ile	Lys	Lys	Asn	Glu	Arg	Leu	Trp	Leu	Leu	Asp	Asp
		20					25							30	
Ser	Lys	Ser	Trp	Trp	Arg	Val	Arg	Asn	Ser	Met	Asn	Lys	Thr	Gly	Phe
	35					40						45			
Val	Pro	Ser	Asn	Tyr	Val	Glu	Arg	Lys							
	50					55									

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Leu	Met	Asn	Pro	Ala	Tyr	Val	Lys	Phe	Asn	Tyr	Met	Ala	Glu	Arg	Glu
1					5				10					15	
Asp	Glu	Leu	Ser	Leu	Ile	Lys	Gly	Thr	Lys	Val	Ile	Val	Met	Glu	Lys
		20					25						30		
Ile	Cys	Ser	Asp	Gly	Trp	Trp	Thr	Gly	Ser	Tyr	Asn	Gly	Gln	Val	Gly
	35						40					45			
Trp	Phe	Pro	Ser	Asn	Tyr	Val	Thr	Glu	Glu						
	50					55									

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

Val	Leu	His	Val	Val	Gln	Ala	Leu	Tyr	Pro	Phe	Ser	Ser	Ser	Asn	Asp
1					5				10					15	
Glu	Glu	Leu	Asn	Phe	Glu	Lys	Gly	Asp	Val	Met	Asp	Val	Ile	Glu	Lys
		20					25						30		
Pro	Glu	Asn	Asp	Pro	Glu	Trp	Trp	Lys	Cys	Arg	Lys	Ile	Asn	Gly	Met
	35					40						45			

Val Gly Leu Val Pro Lys Asn Tyr Val Thr Val Met
50 55 60

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Asp Leu Phe Ser Tyr Gln Ala Leu Tyr Ser Tyr Ile Pro Gln Asn Asp
1 5 10 15

Asp Glu Leu Glu Leu Arg Asp Gly Asp Ile Val Asp Val Met Glu Lys
20 25 30

Cys Asp Asp Gly Trp Phe Val Gly Thr Ser Arg Arg Thr Lys Gln Phe
35 40 45

Gly Thr Phe Pro Gly Asn Tyr Val Lys Pro Leu
50 55

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Gln Gly Arg Lys Glu Arg Ala Arg Tyr Asp Leu Glu Ala Ala Gln Asp
1 5 10 15

Asn Glu Leu Thr Phe Lys Ala Gly Glu Ile Met Thr Val Leu Asp Asp
20 25 30

Ser Asp Pro Asn Trp Trp Lys Gly Glu Arg His Gln Gly Ile Gly Leu
35 40 45

Phe Pro Ser Asn Phe Val Thr Ala Asp
50 55

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Gln Gly Leu Cys Ala Arg Ala Leu Tyr Asp Tyr Gln Ala Ala Asp Asp

1	5	10	15												
Thr	Glu	Ile	Ser	Phe	Asp	Pro	Glu	Asn	Leu	Ile	Thr	Gly	Ile	Glu	Val
		20					25				30				
Ile	Asp	Glu	Gly	Trp	Trp	Arg	Gly	Tyr	Gly	Pro	Asp	Gly	His	Phe	Gly
		35				40				45					
Met	Phe	Pro	Ala	Asn	Tyr	Val	Glu	Leu	Ile						
		50				55									

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

Leu	Val	Leu	Asn	Tyr	Thr	Ala	Leu	Tyr	Pro	Phe	Glu	Ala	Arg	Asn	His
1					5				10					15	
Cys	Glu	Met	Ser	Phe	Asn	Ser	Gly	Asp	Ile	Ile	Gln	Val	Asp	Glu	Lys
					20			25				30			
Thr	Val	Gly	Glu	Pro	Gly	Trp	Leu	Tyr	Gly	Ser	Phe	Gln	Gly	Asn	Phe
					35			40			45				
Gly	Trp	Phe	Pro	Cys	Asn	Tyr	Val	Glu	Lys	Met					
					50			55							

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Val	Glu	Asn	Leu	Lys	Ala	Gln	Ala	Leu	Cys	Ser	Trp	Thr	Ala	Lys	Lys
1					5				10				15		
Asp	Asn	His	Leu	Asn	Phe	Ser	Lys	His	Asp	Ile	Ile	Thr	Val	Leu	Glu
					20			25				30			
Gln	Gln	Glu	Asn	Phe	Trp	Trp	Phe	Gly	Glu	Val	His	Gly	Gly	Arg	Gly
					35			40			45				
Trp	Phe	Pro	Lys	Ser	Tyr	Val	Lys	Ile	Ile						
					50			55							

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Val Gly Glu Glu Tyr Ile Ala Leu Tyr Pro Tyr Ser Ser Val Glu Pro
1 5 10 15

Gly Asp Leu Thr Phe Thr Glu Gly Glu Glu Ile Leu Val Thr Gln Lys
20 25 30

Asp Gly Glu Trp Trp Thr Gly Ser Ile Gly Asp Arg Ser Gly Ile Phe
35 40 45

Pro Ser Asn Tyr Val Lys Pro Lys
50 55

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Lys Pro Glu Ile Ala Gln Val Thr Ser Ala Tyr Val Ala Ser Gly Ser
1 5 10 15

Glu Gln Leu Ser Leu Ala Pro Gly Gln Leu Ile Leu Ile Leu Lys Lys
20 25 30

Asn Thr Ser Gly Trp Trp Gln Gly Glu Leu Gln Ala Arg Gly Lys Lys
35 40 45

Arg Gln Lys Gly Trp Phe Pro Ala Ser Trp Val Lys Leu Leu
50 55 60

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 amino acids
 - (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Pro Val Cys Gln Val Ile Ala Met Tyr Asp Tyr Ala Ala Asn Asn Glu
1 5 10 15

Asp Glu Leu Ser Phe Ser Lys Gly Gln Leu Ile Asn Val Met Asn Lys
20 25 30

Asp Asp Pro Asp Trp Trp Gln Gly Glu Ile Asn Gly Val Thr Gly Leu
35 40 45

Phe Pro Ser Asn Tyr Val Lys Met Thr

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

AATTCAAGCG CGGGGTCTTT AGGATTTGCA GCTCCAGGAA GCGAGATGTC GAAAGCCGCC	60
ACCCAAACCA GTCAAACCAAG GGCAAGTTAA AGTCTTCAGA GCCCTGTATA CGTTTGAACC	120
CAGAACTCCA GATGAATTAT ACTTTGAGGA AGGTGATATT ATCTACATTA CTGACATGAG	180
CGATACCAAT TGGTGGAAAG GCACCTCCAA AGGCAGGACT GGACTAATTC CAAGCAACTA	240
TGTGGCTGAG CAGGCAGAAT CCATTGACAA TCCATTGCAT GAAGCAGCAA AAAGAGGCAA	300
CTTGAGCTGG TTGAGAGAGT GTTGGACAA CAGAGTGGGT GTTAATGGCT TAGACAAACC	360
TGGAAGCACT GCCTTATACT GGGCTTGCCA CGGGGGCCAC AAAGATATAG TGGAAATGCT	420
ATTACTCTA CCAAATATTG AACTGAACCA GCAGAACAAAG TTGGGAGATA CAGCTTGCA	480
TGCTGCTGCC TGGAGGGTT ATGCAGATAT CGTCCAGTTG CTTCTGGCAA AAGGTGCTAG	540
AACAGACTTA AGAAACATTG AGAAGAAGCT GGCCTTCGAC ATGGCTACCA ATGCTGCCTG	600
TGCATCTCTC CTGAAAAAGA AACAGGGAAC AGATGCAGTT CGAACATTAA GCAATGCCGA	660
GGACTATCTC GATGATGAAG ACTCAGATTA A	691

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Asn Ser Ser Ala Gly Ser Leu Gly Phe Ala Ala Pro Gly Ser Glu Met			
1	5	10	15
Ser Lys Pro Pro Pro Lys Pro Val Lys Pro Gly Gln Val Lys Val Phe			
20	25	30	
Arg Ala Leu Tyr Thr Phe Glu Pro Arg Thr Pro Asp Glu Leu Tyr Phe			
35	40	45	
Glu Glu Gly Asp Ile Ile Tyr Ile Thr Asp Met Ser Asp Thr Asn Trp			
50	55	60	
Trp Lys Gly Thr Ser Lys Gly Arg Thr Gly Leu Ile Pro Ser Asn Tyr			
65	70	75	80

Val Ala Glu Gln Ala Glu Ser Ile Asp Asn Pro Leu His Glu Ala Ala
 85 90 95
 Lys Arg Gly Asn Leu Ser Trp Leu Arg Glu Cys Leu Asp Asn Arg Val
 100 105 110
 Gly Val Asn Gly Leu Asp Lys Ala Gly Ser Thr Ala Leu Tyr Trp Ala
 115 120 125
 Cys His Gly Gly His Lys Asp Ile Val Glu Met Leu Phe Thr Gln Pro
 130 135 140
 Asn Ile Glu Leu Asn Gln Gln Asn Lys Leu Gly Asp Thr Ala Leu His
 145 150 155 160
 Ala Ala Ala Trp Lys Gly Tyr Ala Asp Ile Val Gln Leu Leu Leu Ala
 165 170 175
 Lys Gly Ala Arg Thr Asp Leu Arg Asn Ile Glu Lys Lys Leu Ala Phe
 180 185 190
 Asp Met Ala Thr Asn Ala Ala Cys Ala Ser Leu Leu Lys Lys Lys Gln
 195 200 205
 Gly Thr Asp Ala Val Arg Thr Leu Ser Asn Ala Glu Asp Tyr Leu Asp
 210 215 220
 Asp Glu Asp Ser Asp
 225

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Other
 - (D) OTHER INFORMATION: May or may not have carboxy-terminal amide and/or biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Ser Arg Ser Leu Ser Glu Val Ser Pro Lys Pro Pro Ile Arg Ser Val
 1 5 10 15
 Ser Leu Ser Arg
 20

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Other
 - (D) OTHER INFORMATION: May or may not have carboxy-terminal amide and/or biotinylated N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Ser Arg Pro Pro Arg Trp Ser Pro Pro Pro Val Pro Leu Pro Thr Ser
1 5 10 15
Leu Asp Ser Arg
20

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 43..681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

TNNNCACTCA CGTCGGTGGT GTTGGTACGG ATCGATTCAA GCACGAGACG AAGACGGAAC	60
CGGAGCCGGG CGCGCGGACG CGGGACCCGG GTCCTGAGAA AGCCGAAGAT GGCAGTGAAT	120
GTGTACTCTA CGTCAGTCAC CAGTGATAAC CTAAGTCGAC ATGACATGCT GGCTTGGATC	180
AATGAATCTC TGCAGTTGAA TCTGACAAAG ATAGAACAGT TGTGTTCAAGG GGCTGCATAT	240
TGTCAGTTA TGGACATGCT CTTCCCTGGA TCCATTGCCT TGAAGAAAGT GAAATTCCAA	300
GCTAAGCTAG AACATGAATA TATCCAGAAC TTCAAAATAC TACAAGCAGG CTTCAAGAGG	360
ATGGCGTTG ACAAAATAAT TCCTGTGGAT AAATTAGTAA AAGGAAAATT TCAGGACAAT	420
TTTGAATTG TTCAATGGTT CAAGAAGTTT TTTGATGCAA ATTATGATGG AAAAGAGTAT	480
GATCCTGTAG CTGCCAGACA AGGTCAAGAA ACTGCAGTGG NTCCCTCTCT TGTCCGCCA	540
GCTTGAGTA AACCGAAGAA ACCTCTCGGN TCCAGTACTG CAGNCCCACA GAGACCCATT	600
GNAACACAGA GGACTACTGC AGNTCTAAG GNTGGCCCG GAATGGTGGC AAAGAATCCT	660
GGTGTGGNNA ATGGAGGATG ATGANGCAGC TNT	693

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Arg Ile Asp Ser Ser Thr Arg Arg Arg Arg Asn Arg Ser Arg Ala Arg
1 5 10 15

Gly Arg Arg Thr Arg Val Leu Arg Lys Pro Lys Met Ala Val Asn Val
20 25 30

Tyr Ser Thr Ser Val Thr Ser Asp Asn Leu Ser Arg His Asp Met Leu
35 40 45

Ala Trp Ile Asn Glu Ser Leu Asn Leu Gln Leu Thr Lys Ile Glu Gln
50 55 60

Leu Cys Ser Gly Ala Ala Tyr Cys Gln Phe Met Asp Met Leu Phe Pro
65 70 75 80

Gly Ser Ile Ala Leu Lys Lys Val Lys Phe Gln Ala Lys Leu Glu His
85 90 95

Glu Tyr Ile Gln Asn Phe Lys Ile Leu Gln Ala Gly Phe Lys Arg Met
100 105 110

Gly Val Asp Lys Ile Ile Pro Val Asp Lys Leu Val Lys Gly Lys Phe
115 120 125

Gln Asp Asn Phe Glu Phe Val Gln Trp Phe Lys Lys Phe Phe Asp Ala
130 135 140

Asn Tyr Asp Gly Lys Glu Tyr Asp Pro Val Ala Ala Arg Gln Gly Gln
145 150 155 160

Glu Thr Ala Val Xaa Pro Ser Leu Val Ala Pro Ala Leu Ser Lys Pro
165 170 175

Lys Lys Pro Leu Gly Ser Ser Thr Ala Xaa Pro Gln Arg Pro Ile Xaa
180 185 190

Thr Gln Arg Thr Thr Ala Xaa Pro Lys Xaa Gly Pro Gly Met Val Arg
195 200 205

Lys Asn Pro Gly Val Xaa Asn Gly Gly
210 215

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Ser Gly Ser Gly Leu Ala Pro Pro Lys Pro Pro Leu Pro Glu Gly Glu
1 5 10 15

Val

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Gly Asp Gly Tyr Leu Glu Leu Ser Pro
1 5